#9

SEQUENCE LISTING

OIPE JC25
JAN 10 2000
PATENT & TRADEMARK OFFICE

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JAN 10 2000
PATENT & TRADEMARK OFFICE

(1) GENERAL INFORMATION:

(i) APPLICANT: EPELBAUM, SABINE URSULA
FALCO, SAVERIO CARL
MCDEVITT, RAYMOND ERVIN, III

(ii) TITLE OF INVENTION: CHIMERIC GENES AND METHODS FOR INCREASING THE LYSINE CONTENT OF THE SEEDS OF PLANTS

(iii) NUMBER OF SEQUENCES: 132

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
(B) STREET: 1007 MARKET STREET
(C) CITY: WILMINGTON
(D) STATE: DELAWARE
(E) COUNTRY: U.S.A.
(F) ZIP: 19898

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: DISKETTE, 3.50 INCH
(B) COMPUTER: IBM PC COMPATIBLE
(C) OPERATING SYSTEM: MICROSOFT OFFICE 97
(D) SOFTWARE: MICROSOFT WINDOWS 95

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/824,627
(B) FILING DATE: MARCH 27, 1997

(viii) ATTORNEY/AGENT INFORMATION:
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(C) REFERENCE/DOCKET NUMBER: BB-1037-F

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1350 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GCT GAA ATT GTT GTC TCC AAA TTT GGC GGT ACC AGC GTA GCT GAT 48
Met Ala Glu Ile Val Val Ser Lys Phe Gly Gly Thr Ser Val Ala Asp
1 5 10 15

TTT GAC GCC ATG AAC CGC AGC GCT GAT ATT GTG CTT TCT GAT GCC AAC 96
Phe Asp Ala Met Asn Arg Ser Ala Asp Ile Val Leu Ser Asp Ala Asn
20 25 30

GTG CGT TTA GTT GTC CTC TCG GCT TCT GCT GGT ATC ACT AAT CTG CTG 144
Val Arg Leu Val Val Leu Ser Ala Ser Ala Gly Ile Thr Asn Leu Leu
35 40 45

GTC GCT TTA GCT GAA GGA CTG GAA CCT GGC GAG CGA TTC GAA AAA CTC 192
Val Ala Leu Ala Glu Gly Leu Glu Pro Gly Glu Arg Phe Glu Lys Leu
50 55 60

GAC GCT ATC CGC AAC ATC CAG TTT GCC ATT CTG GAA CGT CTG CGT TAC 240
Asp Ala Ile Arg Asn Ile Gln Phe Ala Ile Leu Glu Arg Leu Arg Tyr
65 70 75 80

CCG AAC GTT ATC CGT GAA GAG ATT GAA CGT CTG CTG GAG AAC ATT ACT 288
Pro Asn Val Ile Arg Glu Glu Ile Glu Arg Leu Leu Glu Asn Ile Thr
85 90 95

GTT CTG GCA GAA GCG GCG GCG CTG GCA ACG TCT CCG GCG CTG ACA GAT 336
Val Leu Ala Glu Ala Ala Ala Leu Ala Thr Ser Pro Ala Leu Thr Asp
100 105 110

GAG CTG GTC AGC CAC GGC GAG CTG ATG TCG ACC CTG CTG TTT GTT GAG 384
Glu Leu Val Ser His Gly Glu Leu Met Ser Thr Leu Leu Phe Val Glu
115 120 125

ATC CTG CGC GAA CGC GAT GTT CAG GCA CAG TGG TTT GAT GTA CGT AAA 432
Ile Leu Arg Glu Arg Asp Val Gln Ala Gln Trp Phe Asp Val Arg Lys
130 135 140

GTG ATG CGT ACC AAC GAC CGA TTT GGT CGT GCA GAG CCA GAT ATA GCC 480
Val Met Arg Thr Asn Asp Arg Phe Gly Arg Ala Glu Pro Asp Ile Ala
145 150 155 160

```
GCG CTG GCG GAA CTG GCC GCG CTG CAG CTG CTC CCA CGT CTC AAT GAA    528
Ala Leu Ala Glu Leu Ala Ala Leu Gln Leu Leu Pro Arg Leu Asn Glu
                165                 170                 175

GGC TTA GTG ATC ACC CAG GGA TTT ATC GGT AGC GAA AAT AAA GGT CGT    576
Gly Leu Val Ile Thr Gln Gly Phe Ile Gly Ser Glu Asn Lys Gly Arg
            180                 185                 190

ACA ACG ACG CTT GGC CGT GGA GGC AGC GAT TAT ACG GCA GCC TTG CTG    624
Thr Thr Thr Leu Gly Arg Gly Gly Ser Asp Tyr Thr Ala Ala Leu Leu
        195                 200                 205

GCG GAG GCT TTA CAC GCA TCT CGT GTT GAT ATC TGG ACC GAC GTC CCG    672
Ala Glu Ala Leu His Ala Ser Arg Val Asp Ile Trp Thr Asp Val Pro
    210                 215                 220

GGC ATC TAC ACC ACC GAT CCA CGC GTA GTT TCC GCA GCA AAA CGC ATT    720
Gly Ile Tyr Thr Thr Asp Pro Arg Val Val Ser Ala Ala Lys Arg Ile
225                 230                 235                 240

GAT GAA ATC GCG TTT GCC GAA GCG GCA GAG ATG GCA ACT TTT GGT GCA    768
Asp Glu Ile Ala Phe Ala Glu Ala Ala Glu Met Ala Thr Phe Gly Ala
                245                 250                 255

AAA GTA CTG CAT CCG GCA ACG TTG CTA CCC GCA GTA CGC AGC GAT ATC    816
Lys Val Leu His Pro Ala Thr Leu Leu Pro Ala Val Arg Ser Asp Ile
            260                 265                 270

CCG GTC TTT GTC GGC TCC AGC AAA GAC CCA CGC GCA GGT GGT ACG CTG    864
Pro Val Phe Val Gly Ser Ser Lys Asp Pro Arg Ala Gly Gly Thr Leu
        275                 280                 285

GTG TGC AAT AAA ACT GAA AAT CCG CCG CTG TTC CGC GCT CTG GCG CTT    912
Val Cys Asn Lys Thr Glu Asn Pro Pro Leu Phe Arg Ala Leu Ala Leu
    290                 295                 300

CGT CGC AAT CAG ACT CTG CTC ACT TTG CAC AGC CTG AAT ATG CTG CAT    960
Arg Arg Asn Gln Thr Leu Leu Thr Leu His Ser Leu Asn Met Leu His
305                 310                 315                 320

TCT CGC GGT TTC CTC GCG GAA GTT TTC GGC ATC CTC GCG CGG CAT AAT   1008
Ser Arg Gly Phe Leu Ala Glu Val Phe Gly Ile Leu Ala Arg His Asn
                325                 330                 335

ATT TCG GTA GAC TTA ATC ACC ACG TCA GAA GTG AGC GTG GCA TTA ACC   1056
Ile Ser Val Asp Leu Ile Thr Thr Ser Glu Val Ser Val Ala Leu Thr
            340                 345                 350

CTT GAT ACC ACC GGT TCA ACC TCC ACT GGC GAT ACG TTG CTG ACG CAA   1104
Leu Asp Thr Thr Gly Ser Thr Ser Thr Gly Asp Thr Leu Leu Thr Gln
        355                 360                 365

TCT CTG CTG ATG GAG CTT TCC GCA CTG TGT CGG GTG GAG GTG GAA GAA   1152
Ser Leu Leu Met Glu Leu Ser Ala Leu Cys Arg Val Glu Val Glu Glu
    370                 375                 380
```

```
GGT CTG GCG CTG GTC GCG TTG ATT GGC AAT GAC CTG TCA AAA GCC TGC    1200
Gly Leu Ala Leu Val Ala Leu Ile Gly Asn Asp Leu Ser Lys Ala Cys
385                 390                 395                 400

GCC GTT GGC AAA GAG GTA TTC GGC GTA CTG GAA CCG TTC AAC ATT CGC    1248
Ala Val Gly Lys Glu Val Phe Gly Val Leu Glu Pro Phe Asn Ile Arg
                405                 410                 415

ATG ATT TGT TAT GGC GCA TCC AGC CAT AAC CTG TGC TTC CTG GTG CCC    1296
Met Ile Cys Tyr Gly Ala Ser Ser His Asn Leu Cys Phe Leu Val Pro
            420                 425                 430

GGC GAA GAT GCC GAG CAG GTG GTG CAA AAA CTG CAT AGT AAT TTG TTT    1344
Gly Glu Asp Ala Glu Gln Val Val Gln Lys Leu His Ser Asn Leu Phe
        435                 440                 445

GAG TAA                                                            1350
Glu  *
    450
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GATCCATGGC TGAAATTGTT GTCTCCAAAT TTGGCG 36

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTACCGCCAA ATTTGGAGAC AACAATTTCA GCCATG 36

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 48 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
CCCGGGCCAT GGCTACAGGT TTAACAGCTA AGACCGGAGT AGAGCACT                    48
```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
GATATCGAAT TCTCATTATA GAACTCCAGC TTTTTTC                                37
```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 917 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 3..911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
CC ATG GCT ACA GGT TTA ACA GCT AAG ACC GGA GTA GAG CAC TTC GGC      47
   Met Ala Thr Gly Leu Thr Ala Lys Thr Gly Val Glu His Phe Gly
     1               5                  10                  15

ACC GTT GGA GTA GCA ATG GTT ACT CCA TTC ACG GAA TCC GGA GAC ATC     95
Thr Val Gly Val Ala Met Val Thr Pro Phe Thr Glu Ser Gly Asp Ile
                 20                  25                  30

GAT ATC GCT GCT GGC CGC GAA GTC GCG GCT TAT TTG GTT GAT AAG GGC    143
Asp Ile Ala Ala Gly Arg Glu Val Ala Ala Tyr Leu Val Asp Lys Gly
             35                  40                  45

TTG GAT TCT TTG GTT CTC GCG GGC ACC ACT GGT GAA TCC CCA ACG ACA    191
Leu Asp Ser Leu Val Leu Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr
         50                  55                  60

ACC GCC GCT GAA AAA CTA GAA CTG CTC AAG GCC GTT CGT GAG GAA GTT    239
Thr Ala Ala Glu Lys Leu Glu Leu Leu Lys Ala Val Arg Glu Glu Val
     65                  70                  75

GGG GAT CGG GCG AAG CTC ATC GCC GGT GTC GGA ACC AAC AAC ACG CGG    287
Gly Asp Arg Ala Lys Leu Ile Ala Gly Val Gly Thr Asn Asn Thr Arg
 80                  85                  90                  95
```

```
ACA TCT GTG GAA CTT GCG GAA GCT GCT GCT TCT GCT GGC GCA GAC GGC   335
Thr Ser Val Glu Leu Ala Glu Ala Ala Ala Ser Ala Gly Ala Asp Gly
                100                 105                 110

CTT TTA GTT GTA ACT CCT TAT TAC TCC AAG CCG AGC CAA GAG GGA TTG   383
Leu Leu Val Val Thr Pro Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu
            115                 120                 125

CTG GCG CAC TTC GGT GCA ATT GCT GCA GCA ACA GAG GTT CCA ATT TGT   431
Leu Ala His Phe Gly Ala Ile Ala Ala Ala Thr Glu Val Pro Ile Cys
        130                 135                 140

CTC TAT GAC ATT CCT GGT CGG TCA GGT ATT CCA ATT GAG TCT GAT ACC   479
Leu Tyr Asp Ile Pro Gly Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr
    145                 150                 155

ATG AGA CGC CTG AGT GAA TTA CCT ACG ATT TTG GCG GTC AAG GAC GCC   527
Met Arg Arg Leu Ser Glu Leu Pro Thr Ile Leu Ala Val Lys Asp Ala
160                 165                 170                 175

AAG GGT GAC CTC GTT GCA GCC ACG TCA TTG ATC AAA GAA ACG GGA CTT   575
Lys Gly Asp Leu Val Ala Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu
                180                 185                 190

GCC TGG TAT TCA GGC GAT GAC CCA CTA AAC CTT GTT TGG CTT GCT TTG   623
Ala Trp Tyr Ser Gly Asp Asp Pro Leu Asn Leu Val Trp Leu Ala Leu
            195                 200                 205

GGC GGA TCA GGT TTC ATT TCC GTA ATT GGA CAT GCA GCC CCC ACA GCA   671
Gly Gly Ser Gly Phe Ile Ser Val Ile Gly His Ala Ala Pro Thr Ala
        210                 215                 220

TTA CGT GAG TTG TAC ACA AGC TTC GAG GAA GGC GAC CTC GTC CGT GCG   719
Leu Arg Glu Leu Tyr Thr Ser Phe Glu Glu Gly Asp Leu Val Arg Ala
    225                 230                 235

CGG GAA ATC AAC GCC AAA CTA TCA CCG CTG GTA GCT GCC CAA GGT CGC   767
Arg Glu Ile Asn Ala Lys Leu Ser Pro Leu Val Ala Ala Gln Gly Arg
240                 245                 250                 255

TTG GGT GGA GTC AGC TTG GCA AAA GCT GCT CTG CGT CTG CAG GGC ATC   815
Leu Gly Gly Val Ser Leu Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile
                260                 265                 270

AAC GTA GGA GAT CCT CGA CTT CCA ATT ATG GCT CCA AAT GAG CAG GAA   863
Asn Val Gly Asp Pro Arg Leu Pro Ile Met Ala Pro Asn Glu Gln Glu
            275                 280                 285

CTT GAG GCT CTC CGA GAA GAC ATG AAA AAA GCT GGA GTT CTA TAA TGAGAATTC   918
Leu Glu Ala Leu Arg Glu Asp Met Lys Lys Ala Gly Val Leu  *
        290                 295                 300

     (2)  INFORMATION FOR SEQ ID NO:7:

          (i)  SEQUENCE CHARACTERISTICS:
               (A)  LENGTH:  22 base pairs
               (B)  TYPE:  nucleic acid
```

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTTCCCGTGA CCATGGGCCA TC 22

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CATGGCTGGC TTCCCCACGA GGAAGACCAA CAATGACATT ACCTCCATTG CTAGCAACGG 60

TGGAAGAGTA CAATG 75

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CATGCATTGT ACTCTTCCAC CGTTGCTAGC AATGGAGGTA ATGTCATTGT TGGTCTTCCT 60

CGTGGGGAAG CCAGC 75

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CATGGCTTCC TCAATGATCT CCTCCCCAGC TGTTACCACC GTCAACCGTG CCGGTGCCGG 60

CATGGTTGCT CCATTCACCG GCCTCAAAAG 90

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CATGCTTTTG AGGCCGGTGA ATGGAGCAAC CATGCCGGCA CCGGCACGGT TGACGGTGGT 60

AACAGCTGGG GAGGAGATCA TTGAGGAAGC 90

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCGGTTTGCT GTAATAGGTA CCA 23

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGCTTGGTAC CTATTACAGC AAACCGGCAT G 31

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCTTCCTCAA TGATCTCCTC CCCAGCT 27

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```
CATTGTACTC TTCCACCGTT GCTAGCAA                                          28
```

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..20
(D) OTHER INFORMATION: /product= "synthetic oligonucleotide"
/standard_name= "SM 70"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```
CTGACTCGCT GCGCTCGGTC                                                   20
```

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..24
(D) OTHER INFORMATION: /product= "synthetic oligonucleotide"
/standard_name= "SM 71"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```
TATTTTCTCC TTACGCATCT GTGC                                              24
```

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..27
(D) OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
78"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```
TTCATCGATA GGCGACCACA CCCGTCC                                27
```

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..27
(D) OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
79"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
AATATCGATG CCACGATGCG TCCGGCG                                27
```

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..55

(D) OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
81"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CATGGAGGAG AAGATGAAGG CGATGGAAGA GAAGATGAAG GCGTGATAGG TACCG 55

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..55
(D) OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
80"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AATTCGGTAC CTATCACGCC TTCATCTTCT CTTCCATCGC CTTCATCTTC TCCTC 55

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: Protein
(B) LOCATION: 1..14
(D) OTHER INFORMATION: /label= name
/note= "base gene
[(SSP5)2]"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..21
(D) OTHER INFORMATION: /product= "synthetic oligonucleotide"
/standard_name= "SM 84"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GATGGAGGAG AAGATGAAGG C 21

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..21
(D) OTHER INFORMATION: /product= "synthetic oligonucleotide"
/standard_name= "SM 85"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATCGCCTTCA TCTTCTCCTC C 21

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..21
(D) OTHER INFORMATION: /product= "synthetic oligonucleotide"
/standard_name= "SM 82"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GATGGAGGAG AAGCTGAAGG C 21

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..21
(D) OTHER INFORMATION: /product= "synthetic oligonucleotide"
/standard_name= "SM 83"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATCGCCTTCA GCTTCTCCTC C 21

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```
Met Glu Glu Lys Leu Lys Ala
1               5
```

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```
Met Glu Glu Lys Met Lys Ala
1               5
```

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(B) STRAIN: E. coli
(G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:
(B) CLONE: C15

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 2..151
(D) OTHER INFORMATION: /function= "synthetic storage protein"
/product= "protein"
/gene= "ssp"
/standard_name= "5.7.7.7.7.7.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```
C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG     46
  Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met
    1               5                  10                  15

GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG   94
Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu
                 20                  25                  30

AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAA GAG AAG ATG  142
Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met
            35                  40                  45

AAG GCG TGATAGGTAC CG                                            160
Lys Ala
         50
```

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu
  1               5                  10                  15
```

```
Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys
            20                  25                  30

Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met Lys
        35                  40                  45

Ala
```

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(B) STRAIN: E. coli
(G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:
(B) CLONE: C20

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 2..151
(D) OTHER INFORMATION: /function= "synthetic storage protein"
/product= "protein"
/gene= "ssp"
/standard_name= "5.7.7.7.7.7.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```
C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG      46
  Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met
   1               5                  10                  15

GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG    94
Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu
            20                  25                  30

AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAA GAG AAG ATG   142
Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met
        35                  40                  45

AAG GCG TGATAGGTAC CG                                             160
Lys Ala
    50
```

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu
 1               5                  10                  15

Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys
            20                  25                  30

Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met Lys
        35                  40                  45

Ala
```

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(B) STRAIN: E. coli
(G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:
(B) CLONE: C30

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 2..130
(D) OTHER INFORMATION: /function= "synthetic storage protein"
/product= "protein"
/gene= "ssp"
/standard_name= "5.7.7.7.7.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```
C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG      46
  Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met
   1               5                  10                  15

GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG      94
Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu
                20                  25                  30
```

```
AAG CTG AAG GCG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC CG          139
Lys Leu Lys Ala Met Glu Glu Lys Met Lys Ala
         35                  40
```

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu
 1               5                  10                  15

Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys
            20                  25                  30

Leu Lys Ala Met Glu Glu Lys Met Lys Ala
        35                  40
```

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 97 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(B) STRAIN: E. coli
(G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:
(B) CLONE: D16

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 2..88
(D) OTHER INFORMATION: /function= "synthetic storage protein"
/product= "protein"
/gene= "ssp"
/standard_name= "5.5.5.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```
C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG      46
  Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met
   1               5                  10                  15
```

GAG GAG AAG ATG AAG GCG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC 95
Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala
20 25

CG 97

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu
1 5 10 15

Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala
20 25

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(B) STRAIN: E. coli
(G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:
(B) CLONE: D20

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 2..109
(D) OTHER INFORMATION: /function= "synthetic storage protein"
/product= "protein"
/gene= "ssp"
/standard_name= "5.5.5.5.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG 46
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met
1 5 10 15

```
GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG GAA GAG   94
Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu Glu
                 20                  25                  30

AAG ATG AAG GCG TGATAGGTAC CG                                     118
Lys Met Lys Ala
             35

    (2)   INFORMATION FOR SEQ ID NO:38:

          (i)   SEQUENCE CHARACTERISTICS:
                (A)  LENGTH:  35 amino acids
                (B)  TYPE:  amino acid
                (D)  TOPOLOGY:  linear

         (ii)   MOLECULE TYPE:  protein

         (xi)   SEQUENCE DESCRIPTION:  SEQ ID NO:38:

    Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu
      1               5                  10                  15

    Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys
                 20                  25                  30

    Met Lys Ala
             35

    (2)   INFORMATION FOR SEQ ID NO:39:

          (i)   SEQUENCE CHARACTERISTICS:
                (A)  LENGTH:  97 base pairs
                (B)  TYPE:  nucleic acid
                (C)  STRANDEDNESS:  double
                (D)  TOPOLOGY:  linear

         (ii)   MOLECULE TYPE:  DNA (genomic)

         (vi)   ORIGINAL SOURCE:
                (B)  STRAIN:  E. coli
                (G)  CELL TYPE:  DH5 alpha

        (vii)   IMMEDIATE SOURCE:
                (B)  CLONE:  D33

         (ix)   FEATURE:
                (A)  NAME/KEY:  CDS
                (B)  LOCATION:  2..88
                (D)  OTHER INFORMATION:  /function= "synthetic
                                         storage protein"
                                         /product= "protein"
                                         /gene= "ssp"
                                         /standard_name=
                                         "5.5.5.5"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```
C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG   46
  Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met
   1               5                  10                  15

GAG GAG AAG ATG AAG GCG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC  95
Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala
                20                  25

CG                                                             97
```

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu
 1               5                  10                  15

Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala
            20                  25
```

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..21
(D) OTHER INFORMATION: /product= "synthetic oligonucleotide"
/standard_name= "SM 86"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```
GATGGAGGAG AAGCTGAAGA A                                            21
```

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
    (A) NAME/KEY: misc_feature
    (B) LOCATION: 1..21
    (D) OTHER INFORMATION: /product= "synthetic oligonucleotide"
    /standard_name= "SM 87"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ATCTTCTTCA GCTTCTCCTC C 21

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 21 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
    (A) NAME/KEY: misc_feature
    (B) LOCATION: 1..21
    (D) OTHER INFORMATION: /product= "synthetic oligonucleotide"
    /standard_name= "SM 88"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GATGGAGGAG AAGCTGAAGT G 21

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 21 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
    (A) NAME/KEY: misc_feature
    (B) LOCATION: 1..21
    (D) OTHER INFORMATION: /product= "synthetic oligonucleotide"
    /standard_name= "SM 89"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ATCCACTTCA GCTTCTCCTC C 21

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..21
(D) OTHER INFORMATION: /product= "synthetic oligonucleotide"
/standard_name= "SM 90"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

GATGGAGGAG AAGATGAAGA A 21

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..21
(D) OTHER INFORMATION: /product= "synthetic oligonucleotide"
/standard_name= "SM 91"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ATCTTCTTCA TCTTCTCCTC C 21

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..21

(D) OTHER INFORMATION: /product= "synthetic oligonucleotide"
/standard_name= "SM 92"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

```
GATGGAGGAG AAGATGAAGT G                                              21
```

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..21
(D) OTHER INFORMATION: /product= "synthetic oligonucleotide"
/standard_name= "SM 93"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

```
ATCCACTTCA TCTTCTCCTC C                                              21
```

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

```
Met Glu Glu Lys Leu Lys Lys
1               5
```

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

```
Met Glu Glu Lys Leu Lys Trp
1               5
```

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

```
Met Glu Glu Lys Met Lys Lys
1               5
```

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

```
Met Glu Glu Lys Met Lys Trp
1               5
```

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(B) STRAIN: E. coli
(G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:
(B) CLONE: 82-4

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 2..151
(D) OTHER INFORMATION: /function= "synthetic
storage protein
/product= "protein"

/gene= "ssp"
/standard_name=
"7.7.7.7.7.7.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

```
C ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG     46
  Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met
    1               5                  10                  15

GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG   94
Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu
                 20                  25                  30

AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAA GAG AAG ATG 142
Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met
             35                  40                  45

AAG GCG TGATAGGTAC CG                                            160
Lys Ala
         50
```

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 49 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

```
Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu
  1               5                  10                  15

Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys
             20                  25                  30

Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met Lys
         35                  40                  45

Ala
```

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 97 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(B) STRAIN: E. coli
(G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:
(B) CLONE: 84-H3

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 2..88
(D) OTHER INFORMATION: /function= "synthetic
storage protein
/product= "protein"
/gene= "ssp"
/standard_name=
"5.5.5.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

```
C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG    46
  Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met
    1               5                  10                  15

GAG GAG AAG ATG AAG GCG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC   95
Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala
                 20                  25

CG                                                               97
```

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

```
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu
  1               5                  10                  15

Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala
             20                  25
```

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 97 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(B) STRAIN: E. coli
(G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:
(B) CLONE: 86-H23

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 2..88
(D) OTHER INFORMATION: /function= "synthetic storage protein
/product= "protein"
/gene= "ssp"
/standard_name= "5.8.8.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

```
C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG CTG AAG AAG ATG   46
  Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Lys Met
    1               5                  10                  15

GAG GAG AAG CTG AAG AAG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC  95
Glu Glu Lys Leu Lys Lys Met Glu Glu Lys Met Lys Ala
                 20                  25

CG                                                              97
```

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

```
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Lys Met Glu
  1               5                  10                  15

Glu Lys Leu Lys Lys Met Glu Glu Lys Met Lys Ala
             20                  25
```

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(B) STRAIN: E. coli
(G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:
(B) CLONE: 88-2

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 2..103
(D) OTHER INFORMATION: /function= "synthetic
storage protein
/product= "protein"
/gene= "ssp"
/standard_name=
"5.9.9.9.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

C ATG GAG GAG AAG ATG AAG GCG AAG AAG CTG AAG TGG ATG GAG GAG 46
Met Glu Glu Lys Met Lys Ala Lys Lys Leu Lys Trp Met Glu Glu
1 5 10 15

AAG CTG AAG TGG ATG GAG GAG AAG CTG AAG TGG ATG GAA GAG AAG ATG 94
Lys Leu Lys Trp Met Glu Glu Lys Leu Lys Trp Met Glu Glu Lys Met
20 25 30

AAG GCG TGATAGGTAC CG 112
Lys Ala

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Met Glu Glu Lys Met Lys Ala Lys Lys Leu Lys Trp Met Glu Glu Lys
1 5 10 15

Leu Lys Trp Met Glu Glu Lys Leu Lys Trp Met Glu Glu Lys Met Lys
20 25 30

Ala

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(B) STRAIN: E. coli
(G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:
(B) CLONE: 90-H8

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 2..109
(D) OTHER INFORMATION: /function= "synthetic
storage protein
/product= "protein"
/gene= "ssp"
/standard_name=
"5.10.10.10.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

```
C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG AAG ATG   46
  Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Lys Met
    1               5                  10                   15

GAG GAG AAG ATG AAG AAG ATG GAG GAG AAG ATG AAG AAG ATG GAA GAG 94
Glu Glu Lys Met Lys Lys Met Glu Glu Lys Met Lys Lys Met Glu Glu
                 20                  25                  30

AAG ATG AAG GCG TGATAGGTAC CG                                  118
Lys Met Lys Ala
             35
```

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 35 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

```
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Lys Met Glu
  1               5                  10                  15

Glu Lys Met Lys Lys Met Glu Glu Lys Met Lys Lys Met Glu Glu Lys
             20                  25                  30

Met Lys Ala
         35
```

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 97 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(B) STRAIN: E. coli
(G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:
(B) CLONE: 92-2

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 2..88
(D) OTHER INFORMATION: /function= "synthetic storage protein
/product= "protein"
/gene= "ssp"
/standard_name= "5.11.11.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

```
C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG TGG ATG    46
  Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Trp Met
    1               5                  10                  15

GAG GAG AAG ATG AAG TGG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC   95
Glu Glu Lys Met Lys Trp Met Glu Glu Lys Met Lys Ala
                 20                  25

CG                                                               97
```

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

```
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Trp Met Glu
  1               5                  10                  15

Glu Lys Met Lys Trp Met Glu Glu Lys Met Lys Ala
             20                  25
```

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..84
(D) OTHER INFORMATION: /product= "synthetic oligonucleotide"

/standard_name= "SM
96"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GATGGAGGAA AAGATGAAGG CGATGGAGGA GAAAATGAAA GCTATGGAGG AAAAGATGAA 60

AGCGATGGAG GAGAAAATGA AGGC 84

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..84
(D) OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
97"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ATCGCCTTCA TTTTCTCCTC CATCGCTTTC ATCTTTTCCT CCATAGCTTT CATTTTCTCC 60

TCCATCGCCT TCATCTTTTC CTCC 84

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: Protein
(B) LOCATION: 1..28
(D) OTHER INFORMATION: /label= name
/note= "(SSP 5)4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```
Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu
1               5                   10                  15

Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala
                20                  25
```

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..84
(D) OTHER INFORMATION: /product= "synthetic oligonucleotide"
/standard_name= "SM 98"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```
GATGGAGGAA AAGCTGAAAG CGATGGAGGA GAAACTCAAG GCTATGGAAG AAAAGCTTAA 60

AGCGATGGAG GAGAAACTGA AGGC                                        84
```

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..84
(D) OTHER INFORMATION: /product= "synthetic oligonucleotide"
/standard_name= "SM 99"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```
ATCGCCTTCA GTTTCTCCTC CTACGCTTTA AGCTTTTCTT CCATAGCCTT GAGTTTCTCC 60

TCCATCGCTT TCAGCTTTTC CTCC                                        84
```

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: Protein
(B) LOCATION: 1..28
(D) OTHER INFORMATION: /label= name
/note= "(SSP 7)4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

```
Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu
1               5                   10                  15

Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala
            20                  25
```

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..84
(D) OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
100"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

```
GATGGAGGAA AAGCTTAAGA AGATGGAAGA AAAGCTGAAA TGGATGGAGG AGAAACTCAA 60

AAAGATGGAG GAAAAGCTTA AATG                                        84
```

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..84
(D) OTHER INFORMATION: /product= "synthetic
oligonucleotide"
/standard_name= "SM
101"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

```
ATCCATTTAA GCTTTTCCTC CTACTTTTTG AGTTTCTCCT CCATCCATTT CAGCTTTTCT 60

TCCATCTTCT TAAGCTTTTC CTCC                                        84
```

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

```
Met Glu Glu Lys Leu Lys Lys Met Glu Glu Lys Leu Lys Trp Met Glu
1               5                   10                  15

Glu Lys Leu Lys Lys Met Glu Glu Lys Leu Lys Trp
            20                  25
```

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 243 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(B) STRAIN: E. coli
(G) CELL TYPE: DH5 alpha

(vii) IMMEDIATE SOURCE:
(B) CLONE: 2-9

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 2..235
(D) OTHER INFORMATION: /function= "synthetic
storage protein
/product= "protein"
/gene= "ssp"
/standard_name=
"7.7.7.7.7.7.8.9.8.9.5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```
C ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG      46
  Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met
   1               5                  10                  15
```

```
GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG     94
Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu
                 20                  25                  30

AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAA AAG CTT    142
Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu
             35                  40                  45

AAG AAG ATG GAA GAA AAG CTG AAA TGG ATG GAG GAG AAA CTC AAA AAG    190
Lys Lys Met Glu Glu Lys Leu Lys Trp Met Glu Glu Lys Leu Lys Lys
         50                  55                  60

ATG GAG GAA AAG CTT AAA TGG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC 242
Met Glu Glu Lys Leu Lys Trp Met Glu Glu Lys Met Lys Ala
     65                  70                  75

C                                                                  243
```

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

```
Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu
 1               5                  10                  15

Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys
            20                  25                  30

Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys
        35                  40                  45

Lys Met Glu Glu Lys Leu Lys Trp Met Glu Glu Lys Leu Lys Lys Met
    50                  55                  60

Glu Glu Lys Leu Lys Trp Met Glu Glu Lys Met Lys Ala
65                  70                  75
```

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 175 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(B) STRAIN: E. coli
(G) CELL TYPE: DH5 alpha

```
        (vii)  IMMEDIATE SOURCE:
               (B)  CLONE:  5-1

         (ix)  FEATURE:
               (A)  NAME/KEY:  CDS
               (B)  LOCATION:  2..172
               (D)  OTHER INFORMATION:  /function= "synthetic
                                        storage protein
                                        /product= "protein"
                                        /gene= "ssp"
                                        /standard_name=
                                        "5.5.5.7.7.7.7.5"

         (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO:76:

C ATG GAG GAG AAG ATG AAG GCG ATG GAG GAG AAG ATG AAG GCG ATG     46
  Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met
    1               5                  10                  15

GAG GAG AAG ATG AAG GCG ATG GAG GAA AAG CTG AAA GCG ATG GAG GAG   94
Glu Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu
                20                  25                  30

AAA CTC AAG GCT ATG GAA GAA AAG CTT AAA GCG ATG GAG GAG AAA CTG 142
Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu
            35                  40                  45

AAG GCC ATG GAA GAG AAG ATG AAG GCG TGATAG                       179
Lys Ala Met Glu Glu Lys Met Lys Ala
        50                  55

    (2)  INFORMATION FOR SEQ ID NO:77:

          (i)  SEQUENCE CHARACTERISTICS:
               (A)  LENGTH:  56 amino acids
               (B)  TYPE:  amino acid
               (D)  TOPOLOGY:  linear

         (ii)  MOLECULE TYPE:  protein

         (xi)  SEQUENCE DESCRIPTION:  SEQ ID NO:77:

Met Glu Glu Lys Met Lys Ala Met Glu Glu Lys Met Lys Ala Met Glu
  1               5                  10                  15

Glu Lys Met Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys
              20                  25                  30

Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys
          35                  40                  45

Ala Met Glu Glu Lys Met Lys Ala
      50                  55
```

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(B) STRAIN: E. coli
(G) CELL TYPE: DH5 alpha

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 3..173
(D) OTHER INFORMATION: /function= "synthetic
storage protein
/product= "protein"
/gene= "ssp"
/standard_name=
"SSP-3-5"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

```
CC ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG     47
   Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met
     1               5                  10                  15

GAG GAG AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAG    95
Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu
                 20                  25                  30

AAG CTG AAG GCG ATG GAG GAG AAG CTG AAG GCG ATG GAG GAA AAG ATG   143
Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met
             35                  40                  45

AAG GCG ATG GAA GAG AAG ATG AAG GCG TGATAGGTAC CGAATTC            187
Lys Ala Met Glu Glu Lys Met Lys Ala
         50                  55
```

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

```
Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu
  1               5                  10                  15

Glu Lys Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys
             20                  25                  30
```

Leu Lys Ala Met Glu Glu Lys Leu Lys Ala Met Glu Glu Lys Met Lys
35 40 45

Ala Met Glu Glu Lys Met Lys Ala
50 55

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..61
(D) OTHER INFORMATION: /product= "synthetic oligonucleotide"
/standard_name= "SM 107"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

CATGGAGGAG AAGATGAAAA AGCTCGAAGA GAAGATGAAG GTCATGAAGT GATAGGTACC 60

G 61

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..61
(D) OTHER INFORMATION: /product= "synthetic ligonucleotide"
/standard_name= "SM 106"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

AATTCGGTAC CTATCACTTC ATGACCTTCA TCTTCTCTTC GAGCTTTTTC ATCTTCTCCT 60

C 61

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: Protein
(B) LOCATION: 1..16
(D) OTHER INFORMATION: /label= name
/note= "pSK34 base gene"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

```
Met Glu Glu Lys Met Lys Lys Leu Glu Glu Lys Met Lys Val Met Lys
1               5                   10                  15
```

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..63
(D) OTHER INFORMATION: /product= "synthetic oligonucleotide"
/standard_name= "SM 110"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

```
GCTGGAAGAA AAGATGAAGG CTATGGAGGA CAAGATGAAA TGGCTTGAGG AAAAGATGAA 60

GAA                                                               63
```

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..63
(D) OTHER INFORMATION: /product= "synthetic oligonucleotide"
/standard_name= "SM 111"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

```
AGCTTCTTCA TCTTTTCCTC AAGCCATTTC ATCTTGTCCT CCATAGCCTT CATCTTTTCT 60

TCC                                                               63
```

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

```
Met Glu Glu Lys Met Lys Lys Leu Glu Glu Lys Met Lys Ala Met Glu
  1               5                  10                  15

Asp Lys Met Lys Trp Leu Glu Glu Lys Met Lys Lys Leu Glu Glu Lys
             20                  25                  30

Met Lys Val Met Lys
         35
```

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

```
Met Glu Glu Lys Met Lys Lys Leu Glu Glu Lys Met Lys Ala Met Glu
  1               5                  10                  15

Asp Lys Met Lys Trp Leu Glu Glu Lys Met Lys Lys Leu Glu Glu Lys
             20                  25                  30

Met Lys Val Met Lys
         35
```

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..62
(D) OTHER INFORMATION: /product= "synthetic oligonucletide"
/standard_name= "SM 112"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

```
GCTCGAAGAA AGATGAAGGC AATGGAAGAC AAAATGAAGT GGCTTGAGGA GAAAATGAAG 60

AA                                                                62
```

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..62
(D) OTHER INFORMATION: /product= "synthetic oligonucleotide"
/standard_name= "SM 113"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

```
AGCTTCTTCA TTTTCTCCTC AAGCCACTTC ATTTTGTCTT CCATTGCCTT CATCTTTCTT 60

CG                                                                62
```

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

```
Met Glu Glu Lys Met Lys Lys Leu Lys Glu Glu Met Ala Lys Met Lys
  1             5                  10                  15

Asp Glu Met Trp Lys Leu Lys Glu Glu Met Lys Lys Leu Glu Glu Lys
            20                  25                  30

Met Lys Val Met Lys
        35
```

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..63
(D) OTHER INFORMATION: /product= "synthetic oligonucleotide"
/standard_name= "SM 114"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GCTCAAGGAG GAAATGGCTA AGATGAAAGA CGAAATCTGG AAACTGAAAG AGGAAATGAA 60

GAA 63

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 1..63
(D) OTHER INFORMATION: /product= "synthetic oligonucleotide"
/standard_name= "SM 115"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

AGCTTCTTCA TTTCCTCTTT CAGTTTCCAC ATTTCGTCTT TCATCTTAGC CATTTCCTCC 60

TTG 63

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

```
Met Glu Glu Lys Met Lys Lys Leu Lys Glu Glu Met Ala Lys Met Lys
 1               5                  10                  15

Asp Glu Met Trp Lys Leu Lys Glu Glu Met Lys Lys Leu Glu Glu Lys
            20                  25                  30

Met Lys Val Met Glu Glu Lys Met Lys Lys Leu Glu Glu Lys Met Lys
        35                  40                  45

Ala Met Glu Asp Lys Met Lys Trp Leu Glu Glu Lys Met Lys Lys Leu
    50                  55                  60

Glu Glu Lys Met Lys Val Met Glu Glu Lys Met Lys Lys Leu Glu Glu
65                  70                  75                  80

Lys Met Lys Ala Met Glu Asp Lys Met Lys Trp Leu Glu Glu Lys Met
                85                  90                  95

Lys Lys Leu Glu Glu Lys Met Lys Val Met Lys
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 839 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

```
GGATCCCCCG GGCTGCAGGA ATTCTACGTA CCATATAGTA AGACTTTGTA TATAAGACGT   60

CACCTCTTAC GTGCATGGTT ATATGTGACA TGTGCAGTGA CGTTGTACCA TATAGTAAGA  120

CTTTGTATAT AAGACGTCAC CTCTTACGTG CATGGTTATA TGTGACATGT GCAGTGACGT  180

TAACCGCACC CTCCTTCCCG TCGTTTCCCA TCTCTTCCTC CTTTAGAGCT ACCACTATAT  240

AAATCAGGGC TCATTTTCTC GCTCCTCACA GGCTCATCAG CACCCCGGCA GTGCCACCCC  300

GACTCCCTGC ACCTGCCATG GGTACGCTAG CCCGGGAGAT CTGACAAAGC AGCATTAGTC  360

CGTTGATCGG TGGAAGACCA CTCGTCAGTG TTGAGTTGAA TGTTTGATCA ATAAAATACG  420
```

GCAATGCTGT AAGGGTTGTT TTTTATGCCA TTGATAATAC ACTGTACTGT TCAGTTGTTG 480

AACTCTATTT CTTAGCCATG CCAGTGCTTT TCTTATTTTG AATAACATTA CAGCAAAAAG 540

TTGAAAGACA AAAAAANNNN NCCCCGAACA GAGTGCTTTG GGTCCCAAGC TTCTTTAGAC 600

TGTGTTCGGC GTTCCCCCTA AATTTCTCCC CTATATCTCA CTCACTTGTC ACATCAGCGT 660

TCTCTTTCCC CTATATCTCC ACGCTCTACA GCAGTTCCAC CTATATCAAA CCTCTATACC 720

CCACCACAAC AATATTATAT ACTTTCATCT TCACCTAACT CATGTACCTT CCAATTTTTT 780

TCTACTAATA ATTATTTACG TGCACAGAAA CTTAGGCAAG GGAGAGAGAG AGCGGTACC 839

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CTAGAAGCCT CGGCAACGTC AGCAACGGCG GAAGAATCCG GTG 43

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 43 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

CATGCACCGG ATTCTTCCGC CGTTGCTGAC GTTGCCGAGG CTT 43

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GATCCCATGG CGCCCCTTAA GTCCACCGCC AGCCTCCCCG TCGCCCGCCG CTCCT 55

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CTAGAGGAGC GGCGGGCGAC GGGGAGGCTG GCGGTGGACT TAAGGGGCGC CATGG 55

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

CATGGCGCCC ACCGTGATGA TGGCCTCGTC GGCCACCGCC GTCGCTCCGT TCCAGGGGC 59

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

TTAAGCCCCT GGAACGGAGC GACGGCGGTG GCCGACGAGG CCATCATCAC GGTGGGCGC 59

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GCGCCCACCG TGATGA 16

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

CACCGGATTC TTCCGC 16

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 372 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GTAAGATTGG TAAAGTCCAG CAAGAAAATG AGATAAAAGA GAAGCCTGAA ATGACGAAAA 60

AATCAGGTGT TTTGATTCTT GGTGCTGGAC GTGTGTNTCG CCCAGCTGCT GATTTCCTAG 120

CTTCAGTTAG AACCATTTCG TCACAGCAAT GGTACAAAAC ATATTTCGGA GCAGACTCTG 180

AAGAGAAAAC AGATGTTCAT GTGATTGTCG CGTCTCTGTA TCTTAAGGAT GCCAAAGAGA 240

CGGTTGAAGG TATTTCAGAT GTAGAAGCAG TTCGGCTAGA TGTATCTGAT AGTGAAAGTC 300

TCCTTAAGTA TGTTTCTCAG GTTGATGTTG TCCTAAGTTT ATTACCTGCA AGTTGTCATG 360

CTTGTTGTAG CA 372

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 323 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GGAAGCACAC TGCGACTCTT TTGGAATTCG GGGACATCAA GAATGGACAA ACAACAACCG 60

CTATGGCCAA GACTGTTGGG ATCCCTGCAG CCATTGGAGC TCTGCTGTTA ATTGAAGACA 120

AGATCAAGAC AAGAGGAGTC TTAAGGCCTC TCGAAGCAGA GGTGTATTTG CCAGCTTTGG 180

```
ATATATTGCA AGCATATGGT ATAAAGCTGA TGGAGAAGGC AGAATGATCA AAGAACTCTG    240

TATATTGTTT CTNTCTATAA CTTGGAGTTG GAGACAAAGC TGAAGGAGNC AGNGCCATTA    300

GACCAGCAAA AAAAGGAGGA GGA                                            323
```

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

```
Lys Ile Gly Lys Val Gln Gln Glu Asn Glu Ile Lys Glu Lys Pro Glu
1               5                   10                  15

Met Thr Lys Lys Ser Gly Val Leu Ile Leu Gly Ala Gly Arg Val Xaa
            20                  25                  30

Arg Pro Ala Ala Asp Phe Leu Ala Ser Val Arg Thr Ile Ser Ser Gln
        35                  40                  45

Gln Trp Tyr Lys Thr Tyr Phe Gly Ala Asp Ser Glu Glu Lys Thr Asp
    50                  55                  60

Val His Val Ile Val Ala Ser Leu Tyr Leu Lys Asp Ala Lys Glu Thr
65                  70                  75                  80

Val Glu Gly Ile Ser Asp Val Glu Ala Val Arg Leu Asp Val Ser Asp
                85                  90                  95

Ser Glu Ser Leu Leu Lys Tyr Val Ser Gln Val Asp Val Val Leu Ser
            100                 105                 110

Leu Leu Pro Ala Ser Cys His Ala Cys Cys Ser
        115                 120
```

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

```
Lys His Thr Ala Thr Leu Leu Glu Phe Gly Asp Ile Lys Asn Gly Gln
1               5                   10                  15
```

```
Thr Thr Thr Ala Met Ala Lys Thr Val Gly Ile Pro Ala Ala Ile Gly
            20                  25                  30

Ala Leu Leu Leu Ile Glu Asp Lys Ile Lys Thr Arg Gly Val Leu Arg
        35                  40                  45

Pro Leu Glu Ala Glu Val Tyr Leu Pro Ala Leu Asp Ile Leu Gln Ala
    50                  55                  60

Tyr Gly Ile Lys Leu Met Glu Lys Ala Glu
65                  70
```

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

ATTCCCCATG GTTTCGCCGA CGAAT 25

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CTCTCGGTAC CTAGTACCTA CTGATCAAC 29

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

AGAGAAGCCT GAAATGACGA AAAA 24

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GTCTTGGCCA TAGCGGTTGT TGTT 24

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

TCTAGATGCA CATTCAACTC GAGGTTGTTG CATGATGTTT CATTTACCAA AAAAATCATA 60

GTCAAATTAT GTAAGCAAAT GATATTACAG AAAAGTTTTA CTAGAGAGTT TCAGATTTAC 120

ACATGCACAA CGTTAAAAAA AATAGCAGAA AAAAGAAAGA AGAAAAGTTC TTTATTTGTG 180

AGAAAAATGT ATGAAAAAAA AAGAGATGGG TGTAAAAAGC AAAAGGATAG GACCACTGTT 240

ACTTTGTAGC CTCGTTGAGG AATCTCTTCT CGCATCTCGA CTTTTGTGCC ATTGCAAAGT 300

CAATGCCCAG AACTTGTTCC CAGGCCATCT CCAATTAACT ACGTCTATTT AATTAAACTT 360

TTAAAAGAAA ACCTAATAAA TTAAACAAAA GAAAAGCCGT CAACGAAATC TAAGCTTGCA 420

GCGATATCGA TGAACTGATA CCAAAACAAT GTTCAAGTTT CACTTTCAAA TTGTTTTTTC 480

TTGAAATAGT TTATTGGGTA AGGCCCATAG ATATTTCATA AGAAGAACAC TTGTCGAGGT 540

TGAATCGTAT GTCTGCCCAC CGCGGCCCAT GCATCCTCTG TTGGTAGCAT AATCGTTTTA 600

GGCCATACTA TTGTTCGTAC ACACTGATTT TGAAGTCACC TTTGTGCACT CCTTAATTCC 660

TAAATTGAAG AAGCTTGTTC TCATTCTTCT TTGGGTTACA AATGCCAAGG CAAAAGGAAC 720

TTGGGCCAAA TTAAGACAAC AACTCAAGCC CACTCTCTGC AAATAATACT TGGGAATTTT 780

TACTAAAACG GTGCGTTTCA TCCAAGAATC TATTAATATC CCTAACTTGA AATCATCATA 840

TACGTAACCC AACATATTAA AGAGTTAATA ATGTTAAAAA AAGTCTCAGA AGAGAGAGAC 900

GTAGAGAACA CGGAAAGTGG TAACTGGTAA GCGTCGTCAT CGAGGATATA GTAGCTACGT 960

GAGCAAACGT CTTCACTCAT CTCTGTCTAT TTCTCTTCGA ATACACGTAA TACATTTTCG 1020

ATTGGATTGA TCCTCCCTCG GTCCTATCCA AGTATCCATC CACGTAAACA AGAGCTTGTT 1080

CCTTTCTTGT TTTTTCTTTC TTTAAATAGT AAAAATACTT ATTTCATTTG TTTCGTTTGA 1140

TTTCATTATT ATTGTCTATG GCATTATATA CTATATATAT TATTTCTACA ACATTGGCTG 1200

GCTCACGTTG TTCTCGTGTA TACAACAAAC TTAATTAATG TCTCTCTATT GCATTAGATA 1260

GTTTCGGAGC ATATCCATTA TGTGAAAGCC ACATTAAGTT ATAACTAAAA GTAGTTTTCG 1320

AAAGAGCTTA ATTAAGTTAT GTTCTGTTTC AAATAAAAAT GAACACGAGG GATTTTTTTT 1380

TTTTTTGACA GATCATTATT AACAAAAATG ATTACCTGAA GAAAGGGGAA AATAATTATA 1440

GCTGATTACA GATCATTATT AACAAAAAGA ATTCTTGTCA CATCATTCAT TATAACAAGA 1500

AATATTATAT TATATTAATT TAATCTTTCG CTAACACGCC CACAATATAT TAATCATATA 1560

CGTAATTTAG CTTATAAAAA GGACGGAAAG AGATTATTAC TGCGCCTAAA AAACTCACTA 1620

ATTCCAAAGA AAAAAAAAAG CTTGTATTTT TTCTTGACAA ACCAGCTCAC AGGCATTGCA 1680

TGATCAAACT CATCAGGTAC GTTTTGATTC CTTCTTCCAT AATTTTCCCA TCTTGAGGAA 1740

TGCAAATTTG GAGAGCGCTT TAGCTAAATC ACTGCCTTCA TTTTTTCACT TTGGATTTAA 1800

TAATTTGCAT TCCTCTCTTC CTCTCTGCTC TGTTCTGTTC TGTTCTGTTC TGATTTGAGT 1860

TTTCAATTAA TCGCTCGAGC AAAAGCTATT TCTCAACTCG TTAAATTTCT GTTCCCAGTT 1920

TGTTCGATTT TCAACAGTTT CACATTAAAG TTTGGGTTTT TGATGTTTGG TTGATGAAAC 1980

TCGAAATATG AAATGTTTGT GAATCTATTC CAGGGTGTTT AAAATAAGGG TTTGTTGTTC 2040

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AGAAGTTGGG GAATGGAGTT GTGGGGATTC TAGCTGAAAC AGTTAACAAA TGGGAGAGAC 2160

GAACACCATT GACGCCATCG CATTGCGCTC GCCTTTTACA CGGTGGGAAA GACAGAACCG 2220

GCATTTCCCG CATTGTGGTT CAGCCATCTG CTAAGCGTAT CCATCATGAT GCCTTGTATG 2280

AAGATGTTGG GTGTGAAATT TCTGATGATT TGTCTGATTG TGGGCTTATA CTTGGAATCA 2340

AACAACCTGA GGTGTGGGAA TTTGCATTAA AAAGAGTTCC TTTTTTTCTT CTATATATAT 2400

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CGCTTTCTTT TCACATACTC ATAAGGCACA GAAAGAGAAC ATGCCTTTGT TGGATAAAGT 2520

ATTACACTTT TCATTTATCC TTTTAGTCCT ATCTAAGATA CTGAGGAATG TTGACAAAAG 2580

GGGTATCCAA TTGCAGATTC TTTCTGAGAG AGTGACTTTG TGTGATTATG AGCTCATTGT 2640

TGGGGATCAT GGGAAACGAT TATTGGCGTT TGGTAAATAT GCAGGCAGAG CTGGTCTTGT 2700

TGACTTCTTA CACGGACTTG GACAGCGTAA GCTCATGTTA TAATTCTGAT GATCAGGACA 2760

TGTTTCTGTG CAGAACAAGA TGAGATGTAA TTTTCCATGT TTGATGCAGG ATATCTAAGT 2820

CTAGGATACT CAACACCTTT CCTCTCGCTC GGTGCATCGT ATATGTATTC CTCATTGGCT 2880

GCTGCAAAAG CCGCTGTAAT TTCTGTTGGT GAAGAAATTG CAAGCCAGGG ACTGCCATTA 2940

GGAATCTGCC CTCTTGTATT TGTCTTCACC GGAACAGGAA ATGGTATCTT CTTTAGTTCT 3000

ACTGCGAGTT CTTTGAATCC TTCTGCATAT GTTTCATCTC ATTAAAAAAT TTCTCATCCG 3060

CAGTTTCTCT GGGGGCGCAA GAAATTTTCA AGCTTCTTCC TCACACTTTT GTTGAACCAA 3120

GCAAACTTCC TGAACTATTT GTAAAAGTAA GTCACGCTTT GCTTTTTATT TGGTTTCAGA 3180

GTTTTGAAGA TTCTGAAATG TATATTTCTC ACAGGACAAA GGAATTAGTC AAAATGGGAT 3240

TTCAACAAAG CGAGTCTATC AAGTATATGG TTGTATTATT ACCAGCCAAG ACATGGTTGA 3300

ACACAAAGAT CCATCAAAGT CATTCGACAA AGTAACACTT ACCTTCTTAG CTCCTTGGCT 3360

GTGACTTTTG TTCCACTACG CTAAAGTAGA ATACCTATTA ATTCTTCAAG CTTATGATGT 3420

TTAGGCCGAC TATTATGCAC ACCCGGAACA TTACAATCCA GTTTTCCACG AAAAGATATC 3480

GCCATATACG TCTGTTCTTG GTAGATCCTG ATCACTGTTT TACCTTTAAA GCTCAAGAGT 3540

TTACATATAA GCAAATCCTC TGTCCACTCC GTGACTGTGA CCATCTCATT TTGGTTAGTT 3600

CCAGTGTGTA ACCCCTATGA CTTTCTGTGC AGTAAACTGT ATGTACTGGG AGAAGAGGTT 3660

TCCCTGTCTT CTGAGCACAA AACAGCTTCA AGATTTAACA AAAAAAGGAC TCCCACTAGT 3720

AGGCATATGT GATATAACTT GTGACATCGG TGGCTCCATT GAATTTGTTA ACCGAGCTAC 3780

TTTAATCGAT TCCCCTTTCT TCAGGTAATA TATACTTAGG AAGAGCTTTC TTTTGAGTCA 3840

TCTACGTTTA CTATGATGAA ACTCGTCGAG CTAAACACTA TCTCTAGGTT TAATCCCTCG 3900

AACAATTCAT ACTACGATGA CATGGATGGG GATGGCGTAC TATGCATGGC TGTTGACATT 3960

TTACCCACAG AATTTGCAAA AGAGGTATGT ATGAAGGTTA CAGTTATAGT ACTTAAGATT 4020

AAATCTAAAG TTAAAAACCT TGTATTGAGT GGGAGTTCTT GTGTCCTGAA AAAGGCATCC 4080

CAGCATTTTG GAGATATTCT TTCCGGATTT GTCGGTAGTT TGGCTTCAAT GACTGAAATT 4140

TCAGATCTAC CAGCACATCT GAAGAGGGCT TGCATAAGCT ATAGGGGAGA ATTGACATCT 4200

TTGTATGAGT ATATTCCACG TATGAGGAAG TCAAATCCAG AGTATGTTCT GCTTCGAGCG 4260

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CAACATATTG GTTAGTTTTG ATGAAGAAAG TATATATAAC TAGTTTCCGA ATCATATGAT 4440

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TGGGGCAGAG CGCTGATGCT GAATCGTACT CAGAACTTGA AGTAAGTTTC TTTCTGGATA 4740

AAACCTAATC ATTCACATGG AACAACTGTC AAGAGTTTTT AATGTCACGT TTAGGTTCAA 4800

TGTCCTTTTC ACTAAGTCTC GTAAGTTTTT AAAACAAGTA AACAAACTAC AAGCCAAAAA 4860

CATTCTGGCC CCACATTAAC CTATTCCCAC TTGTTAAAGA ACCCATCTTG CATTATCTTG 4920

GTAGGTTGGT GCGGATGATA AGAGAGTATT GGATCAAATC ATTGATTCAT TAACTCGGTT 4980

AGCTAATCCA AATGAAGATT ATATATCCCC ACATAGAGAA GCAAATAAGA TCTCACTGAA 5040

GATTGGTAAA GTCCAGCAAG AAAATGAGAT AAAAGAGAAG CCTGAAATGA CGAAAAAATC 5100

AGGCGTTTTG ATTCTTGGTG CTGGACGTGT GTGTCGCCCA GCTGCTGATT TCCTAGCTTC 5160

AGTTAGAACC ATTTCGTCAC AGCAATGGTA CAAAACATAT TTCGGAGCAG ACTCTGAAGA 5220

GAAAACAGAT GTTCATGTGA TTGTCGCGTC TCTGTATCTT AAGGATGCCA AAGAGGTAGG 5280

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AACTTCTCTG TTCTTAGATC ACCTTTACTT CAAACTCCAC TGTTCAAATC CATGATCTTA 5520

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ACATTCTTTC AGTAGTTTCC GGTTCCTAAA TGTCTCTGTT TCTTCTTTCT GATTCACTCA 5760

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CATTCCAAGG AGACTGCAGC CAAAGCTGCC AAAACAATTG TGTAAGCTTC TCCATGAAGA 6900

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CTTTTCCAAT TTCCCTTGCA ATTAACTAAA TTGCTCTTCA CGATATGATA TTATACCAAA 8040

ATGGTGATAC CTTGGGAATT GTTAATTTGA CTCATTTGAA CAAATCTCAT CTATAAAATC 8100

ATCCCACCTC TCCACCACAT TTGTTCTCAC TACCAATCAA AAAATAATCT AGTCTTAAAC 8160

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3194 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

ATGAATTCAA ATGGCCATGA GGAGGAGAAG AAGTTGGGGA ATGGAGTTGT GGGGATTCTA 60

TCTGAAACAG TTAACAAATG GGAGAGACGA ACACCATTGA CGCCATCGCA TTGCGCTCGC 120

CTTTTACACG GTGGGAAAGA CAGAACCGGC ATTTCCCGCA TTGTGGTTCA GCCATCTGCT 180

AAGCGTATCC ATCATGATGC CTTGTATGAA CATGTTGGGT GTGAAATTTC TGATGATTTG 240

TCTGATTGTG GGCTTATACT TGGAATCAAA CAACCTGAGC TAGAAATGAT TCTTCCAGAG 300

AGAGCATACG CTTTCTTTTC ACATACTCAT AAGGCACAGA AAGAGAACAT GCCTTTGTTG 360

GATAAAATTC TTTCTGAGAG AGTGACTTTG TGTGATTATG AGCTCATTGT TGGGGATCAT 420

GGGAAACGAT TATTGGCGTT TGGTAAATAT GCAGGCAGAG CTGGTCTTGT TGACTTCTTA 480

CACGGACTTG GACAGCGATA TCTAAGTCTA GGATACTCAA CACCTTTCCT CTCGCTCGGT 540

GCATCGTATA TGTATTCCTC ATTGGCTGCT GCAAAAGCCG CTGTAATTTC TGTTGGTGAA 600

GAAATTGCAA GCCAGGGACT GCCATTAGGA ATCTGCCCTC TTGTATTTGT CTTCACCGGA 660

ACAGGAAATG TTTCTCTGGG GGCGCAAGAA ATTTTCAAGC TTCTTCCTCA CACTTTTGTT 720

GAACCAAGCA AACTTCCTGA ACTATTTGTA AAAGACAAAG GAATTAGTCA AAATGGGATT 780

TCAACAAAGC GAGTCTATCA AGTATATGGT TGTATTATTA CCAGCCAAGA CATGGTTGAA 840

CACAAAGATC CATCAAAGTC ATTCGACAAA GCCGACTATT ATGCACACCC GGAACATTAC 900

AATCCAGTTT TCCACGAAAA GATATCGCCA TATACGTCTG TTCTTGTAAA CTGTATGTAC 960

TGGGAGAAGA GGTTTCCCTG TCTTCTGAGC ACAAAACAGC TTCAAGATTT AACAAAAAAA 1020

GGACTCCCAC TAGTAGGCAT ATGTGATATA ACTTGTGACA TCGGTGGCTC CATTGAATTT 1080

GTTAACCGAG CTACTTTAAT CGATTCCCCT TTCTTCAGGT TTAATCCCTC GAACAATTCA 1140

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TACTACGATG ACATGGATGG GGATGGCGTA CTATGCATGG CTGTTGACAT TTTACCCACA  1200
GAATTTGCAA AAGAGGCATC CCAGCATTTT GGAGATATTC TTTCCGGATT TGTCGGTAGT  1260
TTGGCTTCAA TGACTGAAAT TTCAGATCTA CCAGCACATC TGAAGAGGGC TTGCATAAGC  1320
TATAGGGGAG AATTGACATC TTTGTATGAG TATATTCCAC GTATGAGGAA GTCAAATCCA  1380
GAAGAGGCAC AAGATAATAT TATCGCCAAC GGGGTTTCCA GCCAGAGAAC ATTCAACATA  1440
TTGGTATCTC TGAGCGGACA CCTATTTGAT AAGTTTCTGA TAAACGAAGC TCTTGATATG  1500
ATCGAAGCGG CTGGTGGCTC ATTTCATTTG GCTAAATGTG AACTGGGGCA GAGCGCTGAT  1560
GCTGAATCGT ACTCAGAACT TGAAGTTGGT GCGGATGATA AGAGAGTATT GGATCAAATC  1620
ATTGATTCAT TAACTCGGTT AGCTAATCCA AATGAAGATT ATATATCCCC ACATAGAGAA  1680
GCAAATAAGA TCTCACTGAA GATTGGTAAA GTCCAGCAAG AAAATGAGAT AAAAGAGAAG  1740
CCTGAAATGA CGAAAAAATC AGGTGTTTTG ATTCTTGGTG CTGGACGTGT GTGTCGCCCA  1800
GCTGCTGATT TCCTAGCTTC AGTTAGAACC ATTTCGTCAC AGCAATGGTA CAAAACATAT  1860
TTCGGAGCAG ACTCTGAAGA GAAAACAGAT GTTCATGTGA TTGTCGCGTC TCTGTATCTT  1920
AAGGATGCCA AAGAGACGGT TGAAGGTATT TCAGATGTAG AAGCAGTTCG GCTAGATGTA  1980
TCTGATAGTG AAAGTCTCCT TAAGTATGTT TCTCAGGTTG ATGTTGTCCT AAGTTTATTA  2040
CCTGCAAGTT GTCATGCTGT TGTAGCAAAG ACATGCATTG AGCTGAAGAA GCATCTCGTC  2100
ACTGCTAGCT ATGTTGATGA TGAAACGTCC ATGTTACATG AGAAGGCTAA GAGTGCTGGG  2160
ATAACGATTC TAGGCGAAAT GGGACTGGAC CCTGGAATCG ATCACATGAT GGCGATGAAA  2220
ATGATCAACG ATGCTCATAT CAAAAAAGGG AAAGTGAAGT CTTTTACCTC TTATTGTGGA  2280
GGGCTTCCCT CTCCTGCTGC AGCAAATAAT CCATTAGCAT ATAAATTTAG CTGGAACCCT  2340
GCTGGAGCAA TTCGAGCTGG TCAAAACCCC GCCAAATACA AAAGCAACGG CGACATAATA  2400
CATGTTGATG GGAAGAATCT CTATGATTCC GCGGCAAGAT TCCGAGTACC TAATCTTCCA  2460
GCTTTTGCAT TGGAGTGTTT TCCAAATCGT GACTCCTTGG TTTACGGGGA ACATTATGGC  2520
ATCGAGAGCG AAGCAACAAC GATATTTCGT GGAACACTCA GATATGAAGG GTTTAGTATG  2580
ATAATGGCAA CACTTTCGAA ACTTGGATTC TTTGACAGTG AAGCAAATCA AGTACTCTCC  2640
ACTGGAAAGA GGATTACGTT TGGTGCTCTT TTAAGTAACA TTCTAAATAA GGATGCAGAC  2700
AATGAATCAG AGCCCCTAGC GGGAGAAGAA GAGATAAGCA AGAGAATTAT CAAGCTTGGA  2760
CATTCCAAGG AGACTGCAGC CAAAGCTGCC AAAACAATTG TATTCTTGGG GTTCAACGAA  2820
GAGAGGGAGG TTCCATCACT GTGTAAAAGC GTATTTGATG CAACTTGTTA CCTAATGGAA  2880
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GAGAAACTAG CTTATTCCGG AAATGAACAG GACATGGTGC TTTTGCATCA CGAAGTAGAA 2940

GTGGAATTCC TTGAAAGCAA ACGTATAGAG AAGCACACTG CGACTCTTTT GGAATTCGGG 3000

GACATCAAGA ATGGACAAAC AACAACCGCT ATGGCCAAGA CTGTTGGGAT CCCTGCAGCC 3060

ATTGGAGCTC TGGTGTTAAT TGAAGACAAG ATCAAGACAA GAGGAGTCTT AAGGCCTCTC 3120

GAAGCAGAGG TGTATTTGCC AGCTTTGGAT ATATTGCAAG CATATGGTAT AAAGCTGATG 3180

GAGAAGGCAG AATGA 3195

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1064 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

```
Met Asn Ser Asn Gly His Glu Glu Glu Lys Lys Leu Gly Asn Gly Val
1               5                   10                  15

Val Gly Ile Leu Ser Glu Thr Val Asn Lys Trp Glu Arg Arg Thr Pro
            20                  25                  30

Leu Thr Pro Ser His Cys Ala Arg Leu Leu His Gly Gly Lys Asp Arg
        35                  40                  45

Thr Gly Ile Ser Arg Ile Val Val Gln Pro Ser Ala Lys Arg Ile His
    50                  55                  60

His Asp Ala Leu Tyr Glu His Val Gly Cys Glu Ile Ser Asp Asp Leu
65                  70                  75                  80

Ser Asp Cys Gly Leu Ile Leu Gly Ile Lys Gln Pro Glu Leu Glu Met
                85                  90                  95

Ile Leu Pro Glu Arg Ala Tyr Ala Phe Phe Ser His Thr His Lys Ala
            100                 105                 110

Gln Lys Glu Asn Met Pro Leu Leu Asp Lys Ile Leu Ser Glu Arg Val
        115                 120                 125

Thr Leu Cys Asp Tyr Glu Leu Ile Val Gly Asp His Gly Lys Arg Leu
    130                 135                 140

Leu Ala Phe Gly Lys Tyr Ala Gly Arg Ala Gly Leu Val Asp Phe Leu
145                 150                 155                 160

His Gly Leu Gly Gln Arg Tyr Leu Ser Leu Gly Tyr Ser Thr Pro Phe
                165                 170                 175
```

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Leu Ser Leu Gly Ala Ser Tyr Met Tyr Ser Ser Leu Ala Ala Ala Lys
            180                 185                 190

Ala Ala Val Ile Ser Val Gly Glu Glu Ile Ala Ser Gln Gly Leu Pro
        195                 200                 205

Leu Gly Ile Cys Pro Leu Val Phe Val Phe Thr Gly Thr Gly Asn Val
    210                 215                 220

Ser Leu Gly Ala Gln Glu Ile Phe Lys Leu Leu Pro His Thr Phe Val
225                 230                 235                 240

Glu Pro Ser Lys Leu Pro Glu Leu Phe Val Lys Asp Lys Gly Ile Ser
                245                 250                 255

Gln Asn Gly Ile Ser Thr Lys Arg Val Tyr Gln Val Tyr Gly Cys Ile
            260                 265                 270

Ile Thr Ser Gln Asp Met Val Glu His Lys Asp Pro Ser Lys Ser Phe
        275                 280                 285

Asp Lys Ala Asp Tyr Tyr Ala His Pro Glu His Tyr Asn Pro Val Phe
    290                 295                 300

His Glu Lys Ile Ser Pro Tyr Thr Ser Val Leu Val Asn Cys Met Tyr
305                 310                 315                 320

Trp Glu Lys Arg Phe Pro Cys Leu Leu Ser Thr Lys Gln Leu Gln Asp
                325                 330                 335

Leu Thr Lys Lys Gly Leu Pro Leu Val Gly Ile Cys Asp Ile Thr Cys
            340                 345                 350

Asp Ile Gly Gly Ser Ile Glu Phe Val Asn Arg Ala Thr Leu Ile Asp
        355                 360                 365

Ser Pro Phe Phe Arg Phe Asn Pro Ser Asn Asn Ser Tyr Tyr Asp Asp
    370                 375                 380

Met Asp Gly Asp Gly Val Leu Cys Met Ala Val Asp Ile Leu Pro Thr
385                 390                 395                 400

Glu Phe Ala Lys Glu Ala Ser Gln His Phe Gly Asp Ile Leu Ser Gly
                405                 410                 415

Phe Val Gly Ser Leu Ala Ser Met Thr Glu Ile Ser Asp Leu Pro Ala
            420                 425                 430

His Leu Lys Arg Ala Cys Ile Ser Tyr Arg Gly Glu Leu Thr Ser Leu
        435                 440                 445

Tyr Glu Tyr Ile Pro Arg Met Arg Lys Ser Asn Pro Glu Glu Ala Gln
    450                 455                 460

Asp Asn Ile Ile Ala Asn Gly Val Ser Ser Gln Arg Thr Phe Asn Ile
465                 470                 475                 480
```

```
Leu Val Ser Leu Ser Gly His Leu Phe Asp Lys Phe Leu Ile Asn Glu
                485                 490                 495

Ala Leu Asp Met Ile Glu Ala Ala Gly Gly Ser Phe His Leu Ala Lys
            500                 505                 510

Cys Glu Leu Gly Gln Ser Ala Asp Ala Glu Ser Tyr Ser Glu Leu Glu
        515                 520                 525

Val Gly Ala Asp Asp Lys Arg Val Leu Asp Gln Ile Ile Asp Ser Leu
    530                 535                 540

Thr Arg Leu Ala Asn Pro Asn Glu Asp Tyr Ile Ser Pro His Arg Glu
545                 550                 555                 560

Ala Asn Lys Ile Ser Leu Lys Ile Gly Lys Val Gln Gln Glu Asn Glu
                565                 570                 575

Ile Lys Glu Lys Pro Glu Met Thr Lys Lys Ser Gly Val Leu Ile Leu
            580                 585                 590

Gly Ala Gly Arg Val Cys Arg Pro Ala Ala Asp Phe Leu Ala Ser Val
        595                 600                 605

Arg Thr Ile Ser Ser Gln Gln Trp Tyr Lys Thr Tyr Phe Gly Ala Asp
    610                 615                 620

Ser Glu Glu Lys Thr Asp Val His Val Ile Val Ala Ser Leu Tyr Leu
625                 630                 635                 640

Lys Asp Ala Lys Glu Thr Val Glu Gly Ile Ser Asp Val Glu Ala Val
                645                 650                 655

Arg Leu Asp Val Ser Asp Ser Glu Ser Leu Leu Lys Tyr Val Ser Gln
            660                 665                 670

Val Asp Val Val Leu Ser Leu Leu Pro Ala Ser Cys His Ala Val Val
        675                 680                 685

Ala Lys Thr Cys Ile Glu Leu Lys Lys His Leu Val Thr Ala Ser Tyr
    690                 695                 700

Val Asp Asp Glu Thr Ser Met Leu His Glu Lys Ala Lys Ser Ala Gly
705                 710                 715                 720

Ile Thr Ile Leu Gly Glu Met Gly Leu Asp Pro Gly Ile Asp His Met
                725                 730                 735

Met Ala Met Lys Met Ile Asn Asp Ala His Ile Lys Lys Gly Lys Val
            740                 745                 750

Lys Ser Phe Thr Ser Tyr Cys Gly Gly Leu Pro Ser Pro Ala Ala Ala
        755                 760                 765

Asn Asn Pro Leu Ala Tyr Lys Phe Ser Trp Asn Pro Ala Gly Ala Ile
    770                 775                 780
```

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Arg Ala Gly Gln Asn Pro Ala Lys Tyr Lys Ser Asn Gly Asp Ile Ile
785                 790                 795                 800

His Val Asp Gly Lys Asn Leu Tyr Asp Ser Ala Ala Arg Phe Arg Val
                805                 810                 815

Pro Asn Leu Pro Ala Phe Ala Leu Glu Cys Phe Pro Asn Arg Asp Ser
            820                 825                 830

Leu Val Tyr Gly Glu His Tyr Gly Ile Glu Ser Glu Ala Thr Thr Ile
        835                 840                 845

Phe Arg Gly Thr Leu Arg Tyr Glu Gly Phe Ser Met Ile Met Ala Thr
    850                 855                 860

Leu Ser Lys Leu Gly Phe Phe Asp Ser Glu Ala Asn Gln Val Leu Ser
865                 870                 875                 880

Thr Gly Lys Arg Ile Thr Phe Gly Ala Leu Leu Ser Asn Ile Leu Asn
                885                 890                 895

Lys Asp Ala Asp Asn Glu Ser Glu Pro Leu Ala Gly Glu Glu Glu Ile
            900                 905                 910

Ser Lys Arg Ile Ile Lys Leu Gly His Ser Lys Glu Thr Ala Ala Lys
        915                 920                 925

Ala Ala Lys Thr Ile Val Phe Leu Gly Phe Asn Glu Glu Arg Glu Val
    930                 935                 940

Pro Ser Leu Cys Lys Ser Val Phe Asp Ala Thr Cys Tyr Leu Met Glu
945                 950                 955                 960

Glu Lys Leu Ala Tyr Ser Gly Asn Glu Gln Asp Met Val Leu Leu His
                965                 970                 975

His Glu Val Glu Val Glu Phe Leu Glu Ser Lys Arg Ile Glu Lys His
            980                 985                 990

Thr Ala Thr Leu Leu Glu Phe Gly Asp Ile Lys Asn Gly Gln Thr Thr
        995                 1000                1005

Thr Ala Met Ala Lys Thr Val Gly Ile Pro Ala Ala Ile Gly Ala Leu
    1010                1015                1020

Val Leu Ile Glu Asp Lys Ile Lys Thr Arg Gly Val Leu Arg Pro Leu
1025                1030                1035                1040

Glu Ala Glu Val Tyr Leu Pro Ala Leu Asp Ile Leu Gln Ala Tyr Gly
                1045                1050                1055

Ile Lys Leu Met Glu Lys Ala Glu
            1060
```

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

TTYTCICAYA CICAYAARGC ICA 23

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

TTYTCCCART ACATRCARTT 20

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 619 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GAAAACATGC CTTTGCTGGA TAAGATTCTA GCTGAGAGGG CATCGTTATA TGACTATGAA 60

TTAATTGTTG GGGACACTGG GAAAAGGTTA CTTGCATTTG GAAAATTCGC TGGTAGGGCT 120

GGAATGATCG ACTTTTTGCG CGGATTAGGA CAGCGGTTTT TAAGTCTTGG ATATTCAACA 180

CCTTTCTTGT CACTTGGATC ATCTTACATG TACCCTTCCC TGGCTGCTGC TAAGGCTGCT 240

GTGATTTCTG TTGGTGAAAA ATTGCGACGC AGGGATTGCC ATTGGGGATT TGTCCCCTGG 300

TTTGTTTATT TACTGGTTCA GGAAATGTTT GTTCTGGTGC ACAGGAGATA TTTAAGCTTC 360

TTCCTCATAC CTTTGTTGAT CCATCTAAAC TACGCGACCT ACATAGAACG GACCCAGATC 420

AACCAAGGCA TGCTTCAAAA AGAGTTTTCC AAGTTTATGG TTGTGTTGTG ACTGCCCAAG 480

ACATGGTTGA ACCCAAAGAT CACGTGATAG TGTTTGACAA AGCAGACTAC TATGCACATC 540

CTGAGCATTA CAATCCCACT TTCCATGAAA AAATAGCACC ATATGCATCT GTTATTGTCA 600

ATTGCATGTA TTGGGAAAA 619

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 620 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GAGAATATGC CACTGTTAGA CAAGATCCTT GAAGAAAGGG TGTCCTTGTT TGATTATGAG 60

CTAATTGTTG GAGATGATGG GAAAAGATCA CTAGCATTTG GGAAATTTGC TGGTAGAGCT 120

GGACTGATAG ATTTCTTACA TGGTCTCGGA CAGCGATATT TGAGCCTTGG ATACTCCACT 180

CCATTTCTCT CTCTGGGACA TCTCATATGT TCCTTCGCTC GCTGCAGCCA AGGCTGCAGT 240

CATTGTCGTT GCAGAAGAGA TAGCAACATT TGGACTTCCA TCCGGAATTT GTCCGATAGT 300

GTTTGTGTTC ACTGGAGTTG GAAACGTCTC TCAGGGTGCG CAGGAGATAT TCAAGTTATT 360

GCCCCATACC TTTGTTGATG CTGAGAAGCT TCCCGAAATT TTTCAGGCCA GGAATCTGTC 420

TAAGCAATCT CAGTCGACCA AGAGAGTATT TCAACTTTAT GGTTGTGTTG TGACCTCTAG 480

AGACATAGTT TCTCACAAGG ATCCCACCAG ACAATTTGAC AAAGGTGACT ATTATGCTCA 540

TCCAGAACAC TACACCCCTG TTTTTCATGA AAGAATTGCT CCATATGCAT CTGTCATCGT 600

AAACTGCATG TATTGGGAAA 620

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 206 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

```
Glu Asn Met Pro Leu Leu Asp Lys Ile Leu Ala Glu Arg Ala Ser Leu
1               5                   10                  15

Tyr Asp Tyr Glu Leu Ile Val Gly Asp Thr Gly Lys Arg Leu Leu Ala
            20                  25                  30

Phe Gly Lys Phe Ala Gly Arg Ala Gly Met Ile Asp Phe Leu Arg Gly
        35                  40                  45
```

Leu Gly Gln Arg Phe Leu Ser Leu Gly Tyr Ser Thr Pro Phe Leu Ser
50 55 60

Leu Gly Ser Ser Tyr Met Tyr Pro Ser Leu Ala Ala Ala Lys Ala Ala
65 70 75 80

Val Ile Ser Val Gly Glu Xaa Ile Ala Thr Gln Gly Leu Pro Leu Gly
85 90 95

Ile Cys Pro Leu Val Cys Leu Phe Thr Gly Ser Gly Asn Val Cys Ser
100 105 110

Gly Ala Gln Glu Ile Phe Lys Leu Leu Pro His Thr Phe Val Asp Pro
115 120 125

Ser Lys Leu Arg Asp Leu His Arg Thr Asp Pro Asp Gln Pro Arg His
130 135 140

Ala Ser Lys Arg Val Phe Gln Val Tyr Gly Cys Val Val Thr Ala Gln
145 150 155 160

Asp Met Val Glu Pro Lys Asp His Val Ile Val Phe Asp Lys Ala Asp
165 170 175

Tyr Tyr Ala His Pro Glu His Tyr Asn Pro Thr Phe His Glu Lys Ile
180 185 190

Ala Pro Tyr Ala Ser Val Ile Val Asn Cys Met Tyr Trp Glu
195 200 205

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 207 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Glu Asn Met Pro Leu Leu Asp Lys Ile Leu Glu Glu Arg Val Ser Leu
1 5 10 15

Phe Asp Tyr Glu Leu Ile Val Gly Asp Asp Gly Lys Arg Ser Leu Ala
20 25 30

Phe Gly Lys Phe Ala Gly Arg Ala Gly Leu Ile Asp Phe Leu His Gly
35 40 45

Leu Gly Gln Arg Tyr Leu Ser Leu Gly Tyr Ser Thr Pro Phe Leu Ser
50 55 60

Leu Gly Xaa Ser His Met Xaa Pro Ser Leu Ala Ala Ala Lys Ala Ala
65 70 75 80

```
Val Ile Val Val Ala Glu Glu Ile Ala Thr Phe Gly Leu Pro Ser Gly
                85                  90                  95

Ile Cys Pro Ile Val Phe Val Phe Thr Gly Val Gly Asn Val Ser Gln
            100                 105                 110

Gly Ala Gln Glu Ile Phe Lys Leu Leu Pro His Thr Phe Val Asp Ala
        115                 120                 125

Glu Lys Leu Pro Glu Ile Phe Gln Ala Arg Asn Leu Ser Lys Gln Ser
    130                 135                 140

Gln Ser Thr Lys Arg Val Phe Gln Leu Tyr Gly Cys Val Val Thr Ser
145                 150                 155                 160

Arg Asp Ile Val Ser His Lys Asp Pro Thr Arg Gln Phe Asp Lys Gly
                165                 170                 175

Asp Tyr Tyr Ala His Pro Glu His Tyr Thr Pro Val Phe His Glu Arg
            180                 185                 190

Ile Ala Pro Tyr Ala Ser Val Ile Val Asn Cys Met Tyr Trp Glu
        195                 200                 205
```

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2582 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Glycine max

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 3..2357

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

```
TTGAACCCAA AGATCACGTG ATAGTGTTTG ACAAAGCAGA CTACTATTCA CACCCTGAGC    60
ATTACAATCC CACTTTCCAT GAAAAAATAG CACCATATGC ATCTGTTATT GTCAATTGCA   120
TGTATTGGGA GAAAAGATTT CCTCAATTGC CGAGCTATAA GCAGATGCAA GACTTAATGG   180
GCCGGGGGAG CCCCCTTGTT GGAATAGCTG ACATAACGTG TGATATAGGG GGTTCAATTG   240
AGTTTGTTAA CCGCGGTACT TCAATTGATT CACCCTTCTT CAGATATGAT CCCTTAACAA   300
ATTCCTACCA TGATGATATG GAGGGGAATG GAGTGATATG CTTAGCTGTT GACATTCTTC   360
CAACAGAATT TGCAAAGGAG GCTTCCCAAC ATTTTGGAAA CATACTTTCC CAATTTGTTG   420
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TAAATTTGGC TTCTGCTACA GACATTACAA AGTTGCCTGC TCACTTAAGG AGAGCTTGCA   480
TAGCCCATAA AGGAGTGCTA ACCTCCTTAT ATGATTATAT CCCACGCATG CGGAGTTCTG   540
ATTCAGAGGA AGTATCAGAA AACGCAGAAA ATTCTCTATC CAACAAAAGG AAGTACAATA   600
TATCGGTGTC TCTGAGTGGT CACTTATTTG ATCAGTTTCT GATAAATGAG GCCTTAGATA   660
TTATTGAAGC TGCAGGAGGC TCCTTCCACT TAGTCAACTG CCATGTGGGT CAGAGCATTG   720
AAGCCGTATC ATTCTCTGAA CTTGAAGTTG GTGCAGATAA CAGGGCTGTT CTGGATCAAA   780
TCATTGATTC TTTAACTGCT ATTGCTAGTC CAACTGAACA TGATAGATTT TCAAATCAAG   840
ATTCAAGTAA AATTTCACTT AAGCTTGGTA AAGTTGAAGA GAATGGCATA GAGAAGGAAT   900
CTGACCCCAG AAAGAAGGCT GCGGTTTTAA TTCTTGGAGC TGGTCGGGTC TGTCAACCAG   960
CTGCTGAAAT GTTATCATCA TTTGGAAGGC CATCATCGAG CCAATGGTAT AAAACATTGT  1020
TGGAAGATGA TTTTGAATGT CAAACTGATG TAGAAGTCAT TGTGGGATCT CTGTACCTGA  1080
AGGATGCAGA GCAGACTGTT GAGGGCATTC CAAATGTAAC CGGAATTCAG CTTGATGTGA  1140
TGGATCGTGC CAATTTGTGT AAGTACATTT CACAGGTTGA CGTTGTTATA AGTTTGCTGC  1200
CCCCAAGTTG TCATATTATT GTAGCAAATG CTTGCATTGA GCTGAAAAAA CATCTTGTCA  1260
CTGCTAGCTA TGTTGATAGC TCCATGTCAA TGCTAAATGA TAAGGCTAAA GATGCTGGCA  1320
TAACAATTCT TGGAGAGATG GGCTTGGACC CAGGAATTGG TCATATGATG GCAATGAAGA  1380
TGATCAACCA AGCACATGTG AGGAAGGGGA AAATAAAGTC TTTCACTTCT TATTGTGGTG  1440
GACTTCCATC TCCTGAAGCT GCTAACAATC CATTAGCATA TAAATTCAGT TGGAATCCTG  1500
CAGGAGCCAT CCGAGCTGGG CGCAATCCTG CCACCTACAA ATGGGGTGGT GAAACTGTAC  1560
ATATTGATGG GGACGATCTT TATGATTCGG CTACAAGACT AAGGCTACCG GACCTTCCTG  1620
CTTTTGCTTT GGAATGTCTC CCAAATCGCA ATTCATTACT TTATGGGGAT TTGTATGGAA  1680
TAACTGAAGC ATCAACCATT TTCCGTGGAA CCCTCCGCTA TGAAGGATTT AGTGAGATCA  1740
TGGGGACACT GTCTAGGATT AGCTTATTTA ACAATGAAGC CCATTCGTTG CTAATGAATG  1800
GACAAAGACC AACTTTCAAA AAATTCTTAT TTGAACTTCT CAAAGTTGTT GGTGATAATC  1860
CAGATGAACT ATTGATAGGA GAGAATGACA TCATGGAGCA AATATTAATA CAAGGGCACT  1920
GCAAAGATCA AAGAACGGCA ATGGAGACAG CAAAAACAAT CATTTTCTTG GGACTTCTTG  1980
ACCAAACTGA AATCCCTGCT TCCTGCAAAA GTGCTTTTGA TGTTGCTTGT TTCCGCATGG  2040
AGGAGAGGTT ATCATACACC AGCACAGAAA AGGATATGGT GCTTTTGCAT CATGAAGTGG  2100
AAATAGAATA CCCAGATAGC CAAATTACAG AGAAGCATAG AGCTACTTTA CTTGAATTTG  2160
GGAAGACTCT TGATGAAAAA ACCACAACTG CCATGGCCCT TACTGTTGGT ATTCCAGCTG  2220
CTGTTGGAGC TTTGCTTTTA TTGACAAACA AAATTCAGAC AAGAGGAGTC TTAAGGCCTA  2280
TCGAACCTGA AGTATACAAT CCAGCACTGG ATATTATAGA AGCTTATGGG ATCAAGTTGA  2340
TAGAGAAGAC CGAGTAATTT GCATYTATGA ATTGATGTAT AGGTGTACAT TAATGTACAC  2400
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CATGCAATGT TTGATTTGAA TAAGATAAAA TATAATAATT ACTGCAGTCA TGGAATTGCA 2460

ACTGCCATTC TATGCAACTG TCAGAAATGG ACCACACGGT ACCAGCATAG TTAAAACACT 2520

TAGGCAGATA CCAATTTCAA TTGCAGCAGT ACAATCCAAC CAGTTATGAA GTATGGTTCT 2580

AG 2582

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3265 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Zea mays

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 3..3071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ATTGTGCCCG CCTTCTGCTA GGAGGAGGCA AGAACGGACC TCGAGTAAAC CGGATTATTG 60

TGCAGCCAAG CACAAGGAGG ATCCATCATG ACGCTCAGTA TGAGGATGCA GGATGCGAGA 120

TTTCAGAAGA CCTGTCAGAA TGCGGCCTTA TCATAGGCAT CAAACAACCC AAGCTGCAGA 180

TGATTCTTTC AGATAGAGCG TACGCTTTCT TTTCACACAC ACACAAAGCC CAAAAAGAGA 240

ATATGCCACT GTTAGACAAG ATCCTTGAAG AAAGGGTGTC CTTGTTTGAT TATGAGCTAA 300

TTGTTGGAGA TGATGGGAAA AGATCACTAG CATTTGGGAA ATTTGCTGGT AGAGCTGGAC 360

TGATAGATTT CTTACATGGT CTCGGACAGC GATATTTGAG CCTTGGATAC TCGACTCCAT 420

TTCTCTCTCT GGGACAATCT CATATGTATC CTTCGCTCGC TGCAGCCAAG GCTGCAGTCA 480

TTGTCGTTGC AGAAGAGATA GCAACATTTG GACTTCCATC CGGAATTTGT CCGATAGTGT 540

TTGTGTTCAC TGGAGTTGGA AACGTCTCTC AGGGTGCGCA GGAGATATTC AAGTTATTGC 600

CCCATACCTT TGTTGATGCT GAGAAGCTTC CCGAAATTTT TCAGGCCAGG AATCTGTCTA 660

AGCAATCTCA GTCGACCAAG AGAGTATTTC AACTTTATGG TTGTGTTGTG ACCTCTAGAG 720

ACATAGTTTC TCACAAGGAT CCCACCAGAC AATTTGACAA AGGTGACTAT TATGCTCATC 780

CAGAACACTA CACCCCTGTT TTTCATGAAA GAATTGCTCC ATATGCATCT GTCATCGTAA 840

ACTGTATGTA TTGGGAGAAG AGGTTTCCAC CATTACTAAA TATGGATCAG TTACAGCAAT 900

TGATGGAGAC TGGTTGTCCT TTAGTCGGCG TTTGTGACAT AACTTGTGAT ATTGGAGGTT 960

CCATTGAATT TATCAACAAG AGTACATCAA TAGAGAGGCC TTTCTTTCGG TATGATCCTT 1020

CTAAGAATTC ATACCATGAT GATATGGAAG GTGCCGGAGT GGTCTGCTTG GCTGTTGACA 1080

TTCTCCCTAC AGAATTCTCT AAAGAGGCCT CCCAACATTT TGGAAACATA CTATCTAGAC 1140

TTGTTGCTAG TTTGGCCTCA GTGAAGCAAC CGGCAGAACT TCCTTCCTAC TTGAGAAGAG 1200

CTTGCATTGC ACATGCTGGC AGATTAACTC CTTTGTATGA ATATATCCCT AGGATGAGAA 1260

ATACTATGAT AGATTTGGCA CCCGCAAAAA CAAATCCATT GCCTGACAAG AAGTATAGCA 1320

CCCTGGTATC TCTCAGTGGG CACCTATTTG ATAAGTTCCT TATAAATGAA GCTTTGGACA 1380

TCATTGAGAC AGCTGGAGGT TCATTTCACT TGGTTAGATG TGAAGTTGGA CAAAGCACGG 1440

ATGATATGTC ATACTCAGAG CTTGAAGTAG GAGCAGATGA TACTGCCACA TTGGATAAAA 1500

TTATTGATTC CTTGACTTCT TTAGCTAATG AACATGGTGG AGATCACGAT GCCGGGCAAG 1560

AAATTGAATT AGCTCTGAAG ATAGGAAAAG TCAATGAGTA TGAAACTGAC GTCACAATTG 1620

ATAAAGGAGG GCCAAAGATT TTAATTCTTG GAGCTGGAAG AGTCTGTCGG CCAGCTGCTG 1680

AGTTTCTGGC ATCTTACCCA GACATATGTA CCTATGGTGT TGATGACCAT GATGCAGATC 1740

AAATTCATGT TATCGTGGCA TCTTTGTATC AAAAAGATGC AGAAGAGACA GTTGATGGTA 1800

TTGAAAATAC AACTGCTACC CAGCTTGATG TTGCTGATAT TGGAAGCCTT TCAGATCTTG 1860

TTTCTCAGGT TGAGGTTGTA ATTAGCTTGC TGCCTGCTAG TTTTCATGCT GCCATTGCAG 1920

GAGTATGCAT AGAGTTGAAG AAGCACATGG TAACGGCAAG CTATGTTGAT GAATCCATGT 1980

CAAACTTGAG CCAAGCTGCC AAAGATGCAG GTGTAACTAT ACTTTGTGAA ATGGGCCTAG 2040

ATCCTGGCAT AGATCACTTG ATGTCAATGA AGATGATTGA TGAAGCTCAT GCACGAAAGG 2100

GAAAAATAAA GGCATTTACA TCTTACTGTG GTGGATTGCC ATCTCCAGCT GCAGCAAACA 2160

ATCCGCTTGC CTATAAATTC AGTTGGAACC CAGCTGGTGC ACTCCGGTCA GGGAAAAATC 2220

CTGCAGTCTA CAAATTTCTT GGTGAGACGA TCCATGTAGA TGGTCATAAC TTGTATGAAT 2280

CAGCAAAGAG GCTCAGACTA CGAGAGCTTC CAGCTTTTGC TCTGGAACAC TTGCCAAATC 2340

GGAATTCCTT GATATATGGT GACCTTTATG GTATCTCCAA AGAAGCATCC ACCATATATA 2400

GGGCTACTYT TCGTTACGAA GGTTTTAGTG AGATTATGGT AACCCTTTCC AAAACTGGGT 2460

TCTTTGATGC TGCAAATCAT CCACTGCTGC AAGATACTAG TCGTCCAACA TATAAGGGTT 2520

TCCTTGATGA ACTACTGAAT AATATCTCCA CAATTAACAC GGACTTAGAT ATTGAAGCTT 2580

CTGGTGGATA CGATGATGAC CTGATTGCCA GACTGTTGAA GCTCGGGTGT TGCAAAAATA 2640

AGGAAATAGC TGTTAAGACA GTCAAAACCA TCAAGTTCTT GGGACTACAT GAAGAGACTC 2700

AAATACCTAA GGGTTGTTCG AGCCCATTTG ATGTGATTTG CCAGCGAATG GAACAGAGGA 2760

TGGCCTATGG CCACAATGAG CAAGACATGG TACTGCTCCA CCACGAAGTC GAGGTGGAAT 2820

ACCCGGACGG GCAACCCGCC GAAAAGCACC AAGCGACGCT ACTGGAGTTC GGGAAGGTTG 2880

AAAATGGCAG GTCCACCACT GCCATGGCGC TGACCGTCGG CATTCCAGCA GCAATAGGGG 2940

```
CCCTGCTATT GCTAAAGAAT AAGGTCCAGA CGAAAGGAGT GATCAGGCCT CTGCAACCGG    3000

AAATCTACGT TCCAGCATTG GAGATCTTGG AGTCGTCGGG CATCAAGCTG GTTGAGAAAG    3060

TGGAGACTTG AAAGTTCCCT GATACACAGA TAAAGATAGT ATGATATAGC AGGGCACATG    3120

TATCTTTTGT ATTAACTCCG TTCTGGAATA TATATTTGTG AACTAAAATG TGACAAATAA    3180

AAAGAACGGG TGGAGTATAT TGTAAGAGAC GGCAAAGAAA CCTCTGTATA TATGACCTGT    3240

CGATATCAAA TAATGCCGAT CAGTT                                          3265
```

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 784 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Glycine max

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

```
Glu Pro Lys Asp His Val Ile Val Phe Asp Lys Ala Asp Tyr Tyr Ser
1               5                   10                  15

His Pro Glu His Tyr Asn Pro Thr Phe His Glu Lys Ile Ala Pro Tyr
            20                  25                  30

Ala Ser Val Ile Val Asn Cys Met Tyr Trp Glu Lys Arg Phe Pro Gln
        35                  40                  45

Leu Pro Ser Tyr Lys Gln Met Gln Asp Leu Met Gly Arg Gly Ser Pro
    50                  55                  60

Leu Val Gly Ile Ala Asp Ile Thr Cys Asp Ile Gly Gly Ser Ile Glu
65                  70                  75                  80

Phe Val Asn Arg Gly Thr Ser Ile Asp Ser Pro Phe Phe Arg Tyr Asp
                85                  90                  95

Pro Leu Thr Asn Ser Tyr His Asp Asp Met Glu Gly Asn Gly Val Ile
            100                 105                 110

Cys Leu Ala Val Asp Ile Leu Pro Thr Glu Phe Ala Lys Glu Ala Ser
        115                 120                 125

Gln His Phe Gly Asn Ile Leu Ser Gln Phe Val Val Asn Leu Ala Ser
    130                 135                 140

Ala Thr Asp Ile Thr Lys Leu Pro Ala His Leu Arg Arg Ala Cys Ile
145                 150                 155                 160

Ala His Lys Gly Val Leu Thr Ser Leu Tyr Asp Tyr Ile Pro Arg Met
                165                 170                 175
```

```
Arg Ser Ser Asp Ser Glu Glu Val Ser Glu Asn Ala Glu Asn Ser Leu
            180                 185                 190

Ser Asn Lys Arg Lys Tyr Asn Ile Ser Val Ser Leu Ser Gly His Leu
        195                 200                 205

Phe Asp Gln Phe Leu Ile Asn Glu Ala Leu Asp Ile Ile Glu Ala Ala
    210                 215                 220

Gly Gly Ser Phe His Leu Val Asn Cys His Val Gly Gln Ser Ile Glu
225                 230                 235                 240

Ala Val Ser Phe Ser Glu Leu Glu Val Gly Ala Asp Asn Arg Ala Val
                245                 250                 255

Leu Asp Gln Ile Ile Asp Ser Leu Thr Ala Ile Ala Ser Pro Thr Glu
            260                 265                 270

His Asp Arg Phe Ser Asn Gln Asp Ser Ser Lys Ile Ser Leu Lys Leu
        275                 280                 285

Gly Lys Val Glu Glu Asn Gly Ile Glu Lys Glu Ser Asp Pro Arg Lys
    290                 295                 300

Lys Ala Ala Val Leu Ile Leu Gly Ala Gly Arg Val Cys Gln Pro Ala
305                 310                 315                 320

Ala Glu Met Leu Ser Ser Phe Gly Arg Pro Ser Ser Ser Gln Trp Tyr
                325                 330                 335

Lys Thr Leu Leu Glu Asp Asp Phe Glu Cys Gln Thr Asp Val Glu Val
            340                 345                 350

Ile Val Gly Ser Leu Tyr Leu Lys Asp Ala Glu Gln Thr Val Glu Gly
        355                 360                 365

Ile Pro Asn Val Thr Gly Ile Gln Leu Asp Val Met Asp Arg Ala Asn
    370                 375                 380

Leu Cys Lys Tyr Ile Ser Gln Val Asp Val Val Ile Ser Leu Leu Pro
385                 390                 395                 400

Pro Ser Cys His Ile Ile Val Ala Asn Ala Cys Ile Glu Leu Lys Lys
                405                 410                 415

His Leu Val Thr Ala Ser Tyr Val Asp Ser Ser Met Ser Met Leu Asn
            420                 425                 430

Asp Lys Ala Lys Asp Ala Gly Ile Thr Ile Leu Gly Glu Met Gly Leu
        435                 440                 445

Asp Pro Gly Ile Gly His Met Met Ala Met Lys Met Ile Asn Gln Ala
    450                 455                 460

His Val Arg Lys Gly Lys Ile Lys Ser Phe Thr Ser Tyr Cys Gly Gly
465                 470                 475                 480

Leu Pro Ser Pro Glu Ala Ala Asn Asn Pro Leu Ala Tyr Lys Phe Ser
                485                 490                 495

Trp Asn Pro Ala Gly Ala Ile Arg Ala Gly Arg Asn Pro Ala Thr Tyr
            500                 505                 510
```

```
Lys Trp Gly Gly Glu Thr Val His Ile Asp Gly Asp Asp Leu Tyr Asp
        515                 520                 525

Ser Ala Thr Arg Leu Arg Leu Pro Asp Leu Pro Ala Phe Ala Leu Glu
    530                 535                 540

Cys Leu Pro Asn Arg Asn Ser Leu Leu Tyr Gly Asp Leu Tyr Gly Ile
545                 550                 555                 560

Thr Glu Ala Ser Thr Ile Phe Arg Gly Thr Leu Arg Tyr Glu Gly Phe
                565                 570                 575

Ser Glu Ile Met Gly Thr Leu Ser Arg Ile Ser Leu Phe Asn Asn Glu
            580                 585                 590

Ala His Ser Leu Leu Met Asn Gly Gln Arg Pro Thr Phe Lys Lys Phe
        595                 600                 605

Leu Phe Glu Leu Leu Lys Val Val Gly Asp Asn Pro Asp Glu Leu Leu
    610                 615                 620

Ile Gly Glu Asn Asp Ile Met Glu Gln Ile Leu Ile Gln Gly His Cys
625                 630                 635                 640

Lys Asp Gln Arg Thr Ala Met Glu Thr Ala Lys Thr Ile Ile Phe Leu
                645                 650                 655

Gly Leu Leu Asp Gln Thr Glu Ile Pro Ala Ser Cys Lys Ser Ala Phe
            660                 665                 670

Asp Val Ala Cys Phe Arg Met Glu Glu Arg Leu Ser Tyr Thr Ser Thr
        675                 680                 685

Glu Lys Asp Met Val Leu Leu His His Glu Val Glu Ile Glu Tyr Pro
    690                 695                 700

Asp Ser Gln Ile Thr Glu Lys His Arg Ala Thr Leu Leu Glu Phe Gly
705                 710                 715                 720

Lys Thr Leu Asp Glu Lys Thr Thr Thr Ala Met Ala Leu Thr Val Gly
                725                 730                 735

Ile Pro Ala Ala Val Gly Ala Leu Leu Leu Leu Thr Asn Lys Ile Gln
            740                 745                 750

Thr Arg Gly Val Leu Arg Pro Ile Glu Pro Glu Val Tyr Asn Pro Ala
        755                 760                 765

Leu Asp Ile Ile Glu Ala Tyr Gly Ile Lys Leu Ile Glu Lys Thr Glu
    770                 775                 780
```

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1022 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Zea mays

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

```
Cys Ala Arg Leu Leu Leu Gly Gly Gly Lys Asn Gly Pro Arg Val Asn
1               5                   10                  15

Arg Ile Ile Val Gln Pro Ser Thr Arg Arg Ile His His Asp Ala Gln
            20                  25                  30

Tyr Glu Asp Ala Gly Cys Glu Ile Ser Glu Asp Leu Ser Glu Cys Gly
        35                  40                  45

Leu Ile Ile Gly Ile Lys Gln Pro Lys Leu Gln Met Ile Leu Ser Asp
    50                  55                  60

Arg Ala Tyr Ala Phe Phe Ser His Thr His Lys Ala Gln Lys Glu Asn
65                  70                  75                  80

Met Pro Leu Leu Asp Lys Ile Leu Glu Glu Arg Val Ser Leu Phe Asp
                85                  90                  95

Tyr Glu Leu Ile Val Gly Asp Asp Gly Lys Arg Ser Leu Ala Phe Gly
            100                 105                 110

Lys Phe Ala Gly Arg Ala Gly Leu Ile Asp Phe Leu His Gly Leu Gly
        115                 120                 125

Gln Arg Tyr Leu Ser Leu Gly Tyr Ser Thr Pro Phe Leu Ser Leu Gly
    130                 135                 140

Gln Ser His Met Tyr Pro Ser Leu Ala Ala Ala Lys Ala Ala Val Ile
145                 150                 155                 160

Val Val Ala Glu Glu Ile Ala Thr Phe Gly Leu Pro Ser Gly Ile Cys
                165                 170                 175

Pro Ile Val Phe Val Phe Thr Gly Val Gly Asn Val Ser Gln Gly Ala
            180                 185                 190

Gln Glu Ile Phe Lys Leu Leu Pro His Thr Phe Val Asp Ala Glu Lys
        195                 200                 205

Leu Pro Glu Ile Phe Gln Ala Arg Asn Leu Ser Lys Gln Ser Gln Ser
    210                 215                 220

Thr Lys Arg Val Phe Gln Leu Tyr Gly Cys Val Val Thr Ser Arg Asp
225                 230                 235                 240

Ile Val Ser His Lys Asp Pro Thr Arg Gln Phe Asp Lys Gly Asp Tyr
                245                 250                 255

Tyr Ala His Pro Glu His Tyr Thr Pro Val Phe His Glu Arg Ile Ala
            260                 265                 270

Pro Tyr Ala Ser Val Ile Val Asn Cys Met Tyr Trp Glu Lys Arg Phe
        275                 280                 285

Pro Pro Leu Leu Asn Met Asp Gln Leu Gln Gln Leu Met Glu Thr Gly
    290                 295                 300

Cys Pro Leu Val Gly Val Cys Asp Ile Thr Cys Asp Ile Gly Gly Ser
305                 310                 315                 320

Ile Glu Phe Ile Asn Lys Ser Thr Ser Ile Glu Arg Pro Phe Phe Arg
                325                 330                 335
```

```
Tyr Asp Pro Ser Lys Asn Ser Tyr His Asp Asp Met Glu Gly Ala Gly
            340                 345                 350

Val Val Cys Leu Ala Val Asp Ile Leu Pro Thr Glu Phe Ser Lys Glu
        355                 360                 365

Ala Ser Gln His Phe Gly Asn Ile Leu Ser Arg Leu Val Ala Ser Leu
    370                 375                 380

Ala Ser Val Lys Gln Pro Ala Glu Leu Pro Ser Tyr Leu Arg Arg Ala
385                 390                 395                 400

Cys Ile Ala His Ala Gly Arg Leu Thr Pro Leu Tyr Glu Tyr Ile Pro
                405                 410                 415

Arg Met Arg Asn Thr Met Ile Asp Leu Ala Pro Ala Lys Thr Asn Pro
            420                 425                 430

Leu Pro Asp Lys Lys Tyr Ser Thr Leu Val Ser Leu Ser Gly His Leu
        435                 440                 445

Phe Asp Lys Phe Leu Ile Asn Glu Ala Leu Asp Ile Ile Glu Thr Ala
    450                 455                 460

Gly Gly Ser Phe His Leu Val Arg Cys Glu Val Gly Gln Ser Thr Asp
465                 470                 475                 480

Asp Met Ser Tyr Ser Glu Leu Glu Val Gly Ala Asp Asp Thr Ala Thr
                485                 490                 495

Leu Asp Lys Ile Ile Asp Ser Leu Thr Ser Leu Ala Asn Glu His Gly
            500                 505                 510

Gly Asp His Asp Ala Gly Gln Glu Ile Glu Leu Ala Leu Lys Ile Gly
        515                 520                 525

Lys Val Asn Glu Tyr Glu Thr Asp Val Thr Ile Asp Lys Gly Gly Pro
    530                 535                 540

Lys Ile Leu Ile Leu Gly Ala Gly Arg Val Cys Arg Pro Ala Ala Glu
545                 550                 555                 560

Phe Leu Ala Ser Tyr Pro Asp Ile Cys Thr Tyr Gly Val Asp Asp His
                565                 570                 575

Asp Ala Asp Gln Ile His Val Ile Val Ala Ser Leu Tyr Gln Lys Asp
            580                 585                 590

Ala Glu Glu Thr Val Asp Gly Ile Glu Asn Thr Thr Ala Thr Gln Leu
        595                 600                 605

Asp Val Ala Asp Ile Gly Ser Leu Ser Asp Leu Val Ser Gln Val Glu
    610                 615                 620

Val Val Ile Ser Leu Leu Pro Ala Ser Phe His Ala Ala Ile Ala Gly
625                 630                 635                 640

Val Cys Ile Glu Leu Lys Lys His Met Val Thr Ala Ser Tyr Val Asp
                645                 650                 655

Glu Ser Met Ser Asn Leu Ser Gln Ala Ala Lys Asp Ala Gly Val Thr
            660                 665                 670
```

```
Ile Leu Cys Glu Met Gly Leu Asp Pro Gly Ile Asp His Leu Met Ser
        675                 680                 685

Met Lys Met Ile Asp Glu Ala His Ala Arg Lys Gly Lys Ile Lys Ala
    690                 695                 700

Phe Thr Ser Tyr Cys Gly Gly Leu Pro Ser Pro Ala Ala Ala Asn Asn
705                 710                 715                 720

Pro Leu Ala Tyr Lys Phe Ser Trp Asn Pro Ala Gly Ala Leu Arg Ser
                725                 730                 735

Gly Lys Asn Pro Ala Val Tyr Lys Phe Leu Gly Glu Thr Ile His Val
            740                 745                 750

Asp Gly His Asn Leu Tyr Glu Ser Ala Lys Arg Leu Arg Leu Arg Glu
        755                 760                 765

Leu Pro Ala Phe Ala Leu Glu His Leu Pro Asn Arg Asn Ser Leu Ile
    770                 775                 780

Tyr Gly Asp Leu Tyr Gly Ile Ser Lys Glu Ala Ser Thr Ile Tyr Arg
785                 790                 795                 800

Ala Thr Xaa Arg Tyr Glu Gly Phe Ser Glu Ile Met Val Thr Leu Ser
                805                 810                 815

Lys Thr Gly Phe Phe Asp Ala Ala Asn His Pro Leu Leu Gln Asp Thr
            820                 825                 830

Ser Arg Pro Thr Tyr Lys Gly Phe Leu Asp Glu Leu Leu Asn Asn Ile
        835                 840                 845

Ser Thr Ile Asn Thr Asp Leu Asp Ile Glu Ala Ser Gly Gly Tyr Asp
    850                 855                 860

Asp Asp Leu Ile Ala Arg Leu Leu Lys Leu Gly Cys Cys Lys Asn Lys
865                 870                 875                 880

Glu Ile Ala Val Lys Thr Val Lys Thr Ile Lys Phe Leu Gly Leu His
                885                 890                 895

Glu Glu Thr Gln Ile Pro Lys Gly Cys Ser Ser Pro Phe Asp Val Ile
            900                 905                 910

Cys Gln Arg Met Glu Gln Arg Met Ala Tyr Gly His Asn Glu Gln Asp
        915                 920                 925

Met Val Leu Leu His His Glu Val Glu Val Glu Tyr Pro Asp Gly Gln
    930                 935                 940

Pro Ala Glu Lys His Gln Ala Thr Leu Leu Glu Phe Gly Lys Val Glu
945                 950                 955                 960

Asn Gly Arg Ser Thr Thr Ala Met Ala Leu Thr Val Gly Ile Pro Ala
                965                 970                 975

Ala Ile Gly Ala Leu Leu Leu Leu Lys Asn Lys Val Gln Thr Lys Gly
            980                 985                 990

Val Ile Arg Pro Leu Gln Pro Glu Ile Tyr Val Pro Ala Leu Glu Ile
        995                 1000                1005

Leu Glu Ser Ser Gly Ile Lys Leu Val Glu Lys Val Glu Thr
    1010                1015                1020
```

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1908 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Zea mays

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 3..1908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

```
ATTGTGCCCG CCTTCTGCTA GGAGGAGGCA AGAACGGACC TCGAGTAAAC CGGATTATTG     60
TGCAGCCAAG CACAAGGAGG ATCCATCATG ACGCTCAGTA TGAGGATGCA GGATGCGAGA    120
TTTCAGAAGA CCTGTCAGAA TGCGGCCTTA TCATAGGCAT CAAACAACCC AAGCTGCAGA    180
TGATTCTTTC AGATAGAGCG TACGCTTTCT TTTCACACAC ACACAAAGCC CAAAAAGAGA    240
ATATGCCACT GTTAGACAAG ATCCTTGAAG AAAGGGTGTC CTTGTTTGAT TATGAGCTAA    300
TTGTTGGAGA TGATGGGAAA AGATCACTAG CATTTGGGAA ATTTGCTGGT AGAGCTGGAC    360
TGATAGATTT CTTACATGGT CTCGGACAGC GATATTTGAG CCTTGGATAC TCGACTCCAT    420
TTCTCTCTCT GGGACAATCT CATATGTATC CTTCGCTCGC TGCAGCCAAG GCTGCAGTCA    480
TTGTCGTTGC AGAAGAGATA GCAACATTTG GACTTCCATC CGGAATTTGT CCGATAGTGT    540
TTGTGTTCAC TGGAGTTGGA AACGTCTCTC AGGGTGCGCA GGAGATATTC AAGTTATTGC    600
CCCATACCTT TGTTGATGCT GAGAAGCTTC CCGAAATTTT TCAGGCCAGG AATCTGTCTA    660
AGCAATCTCA GTCGACCAAG AGAGTATTTC AACTTTATGG TTGTGTTGTG ACCTCTAGAG    720
ACATAGTTTC TCACAAGGAT CCCACCAGAC AATTTGACAA AGGTGACTAT TATGCTCATC    780
CAGAACACTA CACCCCTGTT TTTCATGAAA GAATTGCTCC ATATGCATCT GTCATCGTAA    840
ACTGTATGTA TTGGGAGAAG AGGTTTCCAC CATTACTAAA TATGGATCAG TTACAGCAAT    900
TGATGGAGAC TGGTTGTCCT TTAGTCGGCG TTTGTGACAT AACTTGTGAT ATTGGAGGTT    960
CCATTGAATT TATCAACAAG AGTACATCAA TAGAGAGGCC TTTCTTTCGG TATGATCCTT   1020
CTAAGAATTC ATACCATGAT GATATGGAAG GTGCCGGAGT GGTCTGCTTG GCTGTTGACA   1080
TTCTCCCTAC AGAATTCTCT AAAGAGGCCT CCCAACATTT TGGAAACATA CTATCTAGAC   1140
TTGTTGCTAG TTTGGCCTCA GTGAAGCAAC CGGCAGAACT TCCTTCCTAC TTGAGAAGAG   1200
```

CTTGCATTGC ACATGCTGGC AGATTAACTC CTTTGTATGA ATATATCCCT AGGATGAGAA 1260

ATACTATGAT AGATTTGGCA CCCGCAAAAA CAAATCCATT GCCTGACAAG AAGTATAGCA 1320

CCCTGGTATC TCTCAGTGGG CACCTATTTG ATAAGTTCCT TATAAATGAA GCTTTGGACA 1380

TCATTGAGAC AGCTGGAGGT TCATTTCACT TGGTTAGATG TGAAGTTGGA CAAAGCACGG 1440

ATGATATGTC ATACTCAGAG CTTGAAGTAG GAGCAGATGA TACTGCCACA TTGGATAAAA 1500

TTATTGATTC CTTGACTTCT TTAGCTAATG AACATGGTGG AGATCACGAT GCCGGGCAAG 1560

AAATTGAATT AGCTCTGAAG ATAGGAAAAG TCAATGAGTA TGAAACTGAC GTCACAATTG 1620

ATAAAGGAGG GCCAAAGATT TTAATTCTTG GAGCTGGAAG AGTCTGTCGG CCAGCTGCTG 1680

AGTTTCTGGC ATCTTACCCA GACATATGTA CCTATGGTGT TGATGACCAT GATGCAGATC 1740

AAATTCATGT TATCGTGGCA TCTTTGTATC AAAAAGATGC AGAAGAGACA GTTGATGGTA 1800

TTGAAAATAC AACTGCTACC CAGCTTGATG TTGCTGATAT TGGAAGCCTT TCAGATCTTG 1860

TTTCTCAGGT TGAGGTTGTA ATTAGCTTGC TGCCTGCTAG TTTTCATG 1908

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 640 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Zea mays

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Cys Ala Arg Leu Leu Leu Gly Gly Gly Lys Asn Gly Pro Arg Val Asn
1 5 10 15

Arg Ile Ile Val Gln Pro Ser Thr Arg Arg Ile His His Asp Ala Gln
20 25 30

Tyr Glu Asp Ala Gly Cys Glu Ile Ser Glu Asp Leu Ser Glu Cys Gly
35 40 45

Leu Ile Ile Gly Ile Lys Gln Pro Lys Leu Gln Met Ile Leu Ser Asp
50 55 60

Arg Ala Tyr Ala Phe Phe Ser His Thr His Lys Ala Gln Lys Glu Asn
65 70 75 80

Met Pro Leu Leu Asp Lys Ile Leu Glu Glu Arg Val Ser Leu Phe Asp
85 90 95

Tyr Glu Leu Ile Val Gly Asp Asp Gly Lys Arg Ser Leu Ala Phe Gly
100 105 110

```
Lys Phe Ala Gly Arg Ala Gly Leu Ile Asp Phe Leu His Gly Leu Gly
        115                 120                 125

Gln Arg Tyr Leu Ser Leu Gly Tyr Ser Thr Pro Phe Leu Ser Leu Gly
    130                 135                 140

Gln Ser His Met Tyr Pro Ser Leu Ala Ala Ala Lys Ala Ala Val Ile
145                 150                 155                 160

Val Val Ala Glu Glu Ile Ala Thr Phe Gly Leu Pro Ser Gly Ile Cys
                165                 170                 175

Pro Ile Val Phe Val Phe Thr Gly Val Gly Asn Val Ser Gln Gly Ala
            180                 185                 190

Gln Glu Ile Phe Lys Leu Leu Pro His Thr Phe Val Asp Ala Glu Lys
        195                 200                 205

Leu Pro Glu Ile Phe Gln Ala Arg Asn Leu Ser Lys Gln Ser Gln Ser
    210                 215                 220

Thr Lys Arg Val Phe Gln Leu Tyr Gly Cys Val Val Thr Ser Arg Asp
225                 230                 235                 240

Ile Val Ser His Lys Asp Pro Thr Arg Gln Phe Asp Lys Gly Asp Tyr
                245                 250                 255

Tyr Ala His Pro Glu His Tyr Thr Pro Val Phe His Glu Arg Ile Ala
            260                 265                 270

Pro Tyr Ala Ser Val Ile Val Asn Cys Met Tyr Trp Glu Lys Arg Phe
        275                 280                 285

Pro Pro Leu Leu Asn Met Asp Gln Leu Gln Gln Leu Met Glu Thr Gly
    290                 295                 300

Cys Pro Leu Val Gly Val Cys Asp Ile Thr Cys Asp Ile Gly Gly Ser
305                 310                 315                 320

Ile Glu Phe Ile Asn Lys Ser Thr Ser Ile Glu Arg Pro Phe Phe Arg
                325                 330                 335

Tyr Asp Pro Ser Lys Asn Ser Tyr His Asp Asp Met Glu Gly Ala Gly
            340                 345                 350

Val Val Cys Leu Ala Val Asp Ile Leu Pro Thr Glu Phe Ser Lys Glu
        355                 360                 365

Ala Ser Gln His Phe Gly Asn Ile Leu Ser Arg Leu Val Ala Ser Leu
    370                 375                 380

Ala Ser Val Lys Gln Pro Ala Glu Leu Pro Ser Tyr Leu Arg Arg Ala
385                 390                 395                 400

Cys Ile Ala His Ala Gly Arg Leu Thr Pro Leu Tyr Glu Tyr Ile Pro
                405                 410                 415

Arg Met Arg Asn Thr Met Ile Asp Leu Ala Pro Ala Lys Thr Asn Pro
            420                 425                 430

Leu Pro Asp Lys Lys Tyr Ser Thr Leu Val Ser Leu Ser Gly His Leu
        435                 440                 445

Phe Asp Lys Phe Leu Ile Asn Glu Ala Leu Asp Ile Ile Glu Thr Ala
    450                 455                 460
```

```
Gly Gly Ser Phe His Leu Val Arg Cys Glu Val Gly Gln Ser Thr Asp
465                 470                 475                 480

Asp Met Ser Tyr Ser Glu Leu Glu Val Gly Ala Asp Asp Thr Ala Thr
                485                 490                 495

Leu Asp Lys Ile Ile Asp Ser Leu Thr Ser Leu Ala Asn Glu His Gly
            500                 505                 510

Gly Asp His Asp Ala Gly Gln Glu Ile Glu Leu Ala Leu Lys Ile Gly
        515                 520                 525

Lys Val Asn Glu Tyr Glu Thr Asp Val Thr Ile Asp Lys Gly Gly Pro
    530                 535                 540

Lys Ile Leu Ile Leu Gly Ala Gly Arg Val Cys Arg Pro Ala Ala Glu
545                 550                 555                 560

Phe Leu Ala Ser Tyr Pro Asp Ile Cys Thr Tyr Gly Val Asp Asp His
                565                 570                 575

Asp Ala Asp Gln Ile His Val Ile Val Ala Ser Leu Tyr Gln Lys Asp
            580                 585                 590

Ala Glu Glu Thr Val Asp Gly Ile Glu Asn Thr Thr Ala Thr Gln Leu
        595                 600                 605

Asp Val Ala Asp Ile Gly Ser Leu Ser Asp Leu Val Ser Gln Val Glu
    610                 615                 620

Val Val Ile Ser Leu Leu Pro Ala Ser Phe His Ala Ala Ile Ala Gly
625                 630                 635                 640
```

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 720 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Oryza sativa

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 2..720 .

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 215
(D) OTHER INFORMATION: /label= unknown

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 678
(D) OTHER INFORMATION: /label= unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GTTTAAACAT CTTTCCAATC TTGTTTCTCA GGTTGAAGTA GTAGTTAGCT TGCTGCCTGC 60
CAGTTTTCAT GCTGCCATAG CAAGAGTATG CATAGAGATG AAGAAGCACT TGGTCACTGC 120
AAGCTATGTT GATGAGTCCA TGTCAAAGTT GGAACAATCT GCAGAAGGTG CTGGTGTAAC 180
TATTCTCTGT GAAATGGGCC TGGATCCTGG CATANATCAT ATGATGTCAA TGAAGATGAT 240
TGACGAAGCA CATTCACGGA AGGGGAAAAT AAAGTCATTT ACATCCTTTT GTGGAGGACT 300
TCCATCTCCA GCTTCTGCAA ACAATCCACT TGCTTATAAG TTCAGTTGGA GTCCAGCTGG 360
TGCCATCCGT GCAGGGAGAA ACCCTGCTGT CTACAAATTT CATGGAGAAA TCATCCATGT 420
AGATGGTGAT AAATTGTATG AATCCGCAAA GAGGCTCAGA TTACMAGAAC TTCCAGCTTT 480
TGCACTGGAA CACTTGCCAA ACCGGAATTC CTTGATGTAT GGAGACCTGT ATGGGATCTC 540
CAAAGAAGCA TCTACTGTGT ACAGGGCTAC TCTTCGTTAT GAAGGATTTA ATGAGATAAT 600
GGCAACCTTC GCGAAAATTG GGTTTTTTGA TGCTGCAAGT CATCCACTGT TGCAACAAAC 660
TACTCGCCCT ACATACANGG ATTTCCTGTT GAACCCTCAA TGCTTGTACA TCTCCAAAAC 720

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 239 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Oryza sativa

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

```
Phe Lys His Leu Ser Asn Leu Val Ser Gln Val Glu Val Val Val Ser
1               5                   10                  15

Leu Leu Pro Ala Ser Phe His Ala Ala Ile Ala Arg Val Cys Ile Glu
            20                  25                  30

Met Lys Lys His Leu Val Thr Ala Ser Tyr Val Asp Glu Ser Met Ser
        35                  40                  45

Lys Leu Glu Gln Ser Ala Glu Gly Ala Gly Val Thr Ile Leu Cys Glu
    50                  55                  60

Met Gly Leu Asp Pro Gly Ile Xaa His Met Met Ser Met Lys Met Ile
65                  70                  75                  80

Asp Glu Ala His Ser Arg Lys Gly Lys Ile Lys Ser Phe Thr Ser Phe
                85                  90                  95
```

```
Cys Gly Gly Leu Pro Ser Pro Ala Ser Ala Asn Asn Pro Leu Ala Tyr
            100                 105                 110

Lys Phe Ser Trp Ser Pro Ala Gly Ala Ile Arg Ala Gly Arg Asn Pro
        115                 120                 125

Ala Val Tyr Lys Phe His Gly Glu Ile Ile His Val Asp Gly Asp Lys
    130                 135                 140

Leu Tyr Glu Ser Ala Lys Arg Leu Arg Leu Xaa Glu Leu Pro Ala Phe
145                 150                 155                 160

Ala Leu Glu His Leu Pro Asn Arg Asn Ser Leu Met Tyr Gly Asp Leu
                165                 170                 175

Tyr Gly Ile Ser Lys Glu Ala Ser Thr Val Tyr Arg Ala Thr Leu Arg
            180                 185                 190

Tyr Glu Gly Phe Asn Glu Ile Met Ala Thr Phe Ala Lys Ile Gly Phe
        195                 200                 205

Phe Asp Ala Ala Ser His Pro Leu Leu Gln Gln Thr Thr Arg Pro Thr
    210                 215                 220

Tyr Xaa Asp Phe Leu Leu Asn Pro Gln Cys Leu Tyr Ile Ser Lys
225                 230                 235
```

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 308 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Oryza sativa

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

```
CTGCTGTTGC TCCAGAACAA GATCCAAAAG AAAGGAGTGA TCAGGCCTCT GGAACCTGAA    60
ATTTACATTC CAGCGTTGGA GATCTTGGAG TCATCGGGTA TCAAGCTGGC GGAGAGAGTG   120
GAGACCTGAG AATCGGACCC AATATGTATA ATGTAGCATG GTGGTAGCTT CTCTATATAT   180
ATGCTTCAGT GAATAATTGA TTTGCCGTTG TGTGGTAATT AAGCAATGCC CGCTAATAAA   240
TTGTACCGTA GAAGTCCTTC TATGTACATC CGTATCAAAA AATAAAAAAA GCATCGATTA   300
GCTTGAAT                                                            308
```

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Oryza sativa

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

```
Leu Leu Leu Leu Gln Asn Lys Ile Gln Lys Lys Gly Val Ile Arg Pro
1               5                   10                  15

Leu Glu Pro Glu Ile Tyr Ile Pro Ala Leu Glu Ile Leu Glu Ser Ser
            20                  25                  30

Gly Ile Lys Leu Ala Glu Arg Val Glu Thr
        35                  40
```

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 429 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Triticum aestivum

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..252

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 172
(D) OTHER INFORMATION: /label= unknown

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 186
(D) OTHER INFORMATION: /label= unknown

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 331
(D) OTHER INFORMATION: /label= unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

```
TACCCCGACG GGGACCCCAC CGAGAAGCAC CAAGCGACGC TGCTGGAGTT CGGAAAGACC     60
GAGAACGGCA GGCCCACCAC CGCCATGGCC CTCACCGTTG GGGTACCGGC AGCGATAGGA    120
GCCCTGCTCT TGCTCCAGAA CAAGGTCCAG AGGAAAGGGG TGATCCGGCC TNTGGAACCG    180
GAGATNTACA TCCCTGCGCT GGAGATCTTG GAAGCGTCGG GCATCAAGCT GATCGAGAGA    240
GTGGAGACCT GAGGATGTCA GGATGGGATG AGAATCTATC GAGTATATAT GCTGCAGCAA    300
CAGAGGCAGT GAGTAAATAA AATGATGATT NTCGCCGTTG TAAGTAAAAT GAGTGGACTG    360
TATGTATGTA TGTGACTATC TATTGTACTA CATATATACC AAATCTGTCG CCGGTTGATT    420
CTGTTGGTG                                                            429
```

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Triticum aestivum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

```
Tyr Pro Asp Gly Asp Pro Thr Glu Lys His Gln Ala Thr Leu Leu Glu
1               5                   10                  15

Phe Gly Lys Thr Glu Asn Gly Arg Pro Thr Thr Ala Met Ala Leu Thr
            20                  25                  30

Val Gly Val Pro Ala Ala Ile Gly Ala Leu Leu Leu Leu Gln Asn Lys
        35                  40                  45

Val Gln Arg Lys Gly Val Ile Arg Pro Xaa Glu Pro Glu Xaa Tyr Ile
    50                  55                  60

Pro Ala Leu Glu Ile Leu Glu Ala Ser Gly Ile Lys Leu Ile Glu Arg
65                  70                  75                  80

Val Glu Thr
```

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1449 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

```
ATGACGAAAA AATCAGGTGT TTTGATTCTT GGTGCTGGAC GTGTGTGTCG CCCAGCTGCT     60
GATTTCCTAG CTTCAGTTAG AACCATTTCG TCACAGCAAT GGTACAAAAC ATATTTCGGA    120
GCAGACTCTG AAGAGAAAAC AGATGTTCAT GTGATTGTCG CGTCTCTGTA TCTTAAGGAT    180
GCCAAAGAGA CGGTTGAAGG TATTTCAGAT GTAGAAGCAG TTCGGCTAGA TGTATCTGAT    240
AGTGAAAGTC TCCTTAAGTA TGTTTCTCAG GTTGATGTTG TCCTAAGTTT ATTACCTGCA    300
AGTTGTCATG CTGTTGTAGC AAAGACATGC ATTGAGCTGA AGAAGCATCT CGTCACTGCT    360
AGCTATGTTG ATGATGAAAC GTCCATGTTA CATGAGAAGG CTAAGAGTGC TGGGATAACG    420
ATTCTAGGCG AAATGGGACT GGACCCTGGA ATCGATCACA TGATGGCGAT GAAAATGATC    480
AACGATGCTC ATATCAAAAA AGGGAAAGTG AAGTCTTTTA CCTCTTATTG TGGAGGGCTT    540
CCCTCTCCTG CTGCAGCAAA TAATCCATTA GCATATAAAT TTAGCTGGAA CCCTGCTGGA    600
GCAATTCGAG CTGGTCAAAA CCCCGCCAAA TACAAAAGCA ACGGCGACAT AATACATGTT    660
GATGGGAAGA ATCTCTATGA TTCCGCGGCA AGATTCCGAG TACCTAATCT TCCAGCTTTT    720
GCATTGGAGT GTTTTCCAAA TCGTGACTCC TTGGTTTACG GGGAACATTA TGGCATCGAG    780
AGCGAAGCAA CAACGATATT TCGTGGAACA CTCAGATATG AAGGGTTTAG TATGATAATG    840
GCAACACTTT CGAAACTTGG ATTCTTTGAC AGTGAAGCAA ATCAAGTACT CTCCACTGGA    900
AAGAGGATTA CGTTTGGTGC TCTTTTAAGT AACATTCTAA ATAAGGATGC AGACAATGAA    960
TCAGAGCCCC TAGCGGGAGA AGAAGAGATA AGCAAGAGAA TTATCAAGCT TGGACATTCC   1020
AAGGAGACTG CAGCCAAAGC TGCCAAAACA ATTGTATTCT TGGGGTTCAA CGAAGAGAGG   1080
GAGGTTCCAT CACTGTGTAA AAGCGTATTT GATGCAACTT GTTACCTAAT GGAAGAGAAA   1140
CTAGCTTATT CCGGAAATGA ACAGGACATG GTGCTTTTGC ATCACGAAGT AGAAGTGGAA   1200
TTCCTTGAAA GCAAACGTAT AGAGAAGCAC ACTGCGACTC TTTTGGAATT CGGGGACATC   1260
AAGAATGGAC AAACAACAAC CGCTATGGCC AAGACTGTTG GGATCCCTGC AGCCATTGGA   1320
GCTCTGGTGT TAATTGAAGA CAAGATCAAG ACAAGAGGAG TCTTAAGGCC TCTCGAAGCA   1380
GAGGTGTATT TGCCAGCTTT GGATATATTG CAAGCATATG GTATAAAGCT GATGGAGAAG   1440
GCAGAATGA                                                           1449
```

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 482 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

```
Met Thr Lys Lys Ser Gly Val Leu Ile Leu Gly Ala Gly Arg Val Cys
1               5                   10                  15

Arg Pro Ala Ala Asp Phe Leu Ala Ser Val Arg Thr Ile Ser Ser Gln
            20                  25                  30

Gln Trp Tyr Lys Thr Tyr Phe Gly Ala Asp Ser Glu Glu Lys Thr Asp
        35                  40                  45

Val His Val Ile Val Ala Ser Leu Tyr Leu Lys Asp Ala Lys Glu Thr
    50                  55                  60

Val Glu Gly Ile Ser Asp Val Glu Ala Val Arg Leu Asp Val Ser Asp
65                  70                  75                  80

Ser Glu Ser Leu Leu Lys Tyr Val Ser Gln Val Asp Val Val Leu Ser
                85                  90                  95

Leu Leu Pro Ala Ser Cys His Ala Val Val Ala Lys Thr Cys Ile Glu
            100                 105                 110

Leu Lys Lys His Leu Val Thr Ala Ser Tyr Val Asp Asp Glu Thr Ser
        115                 120                 125

Met Leu His Glu Lys Ala Lys Ser Ala Gly Ile Thr Ile Leu Gly Glu
    130                 135                 140

Met Gly Leu Asp Pro Gly Ile Asp His Met Met Ala Met Lys Met Ile
145                 150                 155                 160

Asn Asp Ala His Ile Lys Lys Gly Lys Val Lys Ser Phe Thr Ser Tyr
                165                 170                 175

Cys Gly Gly Leu Pro Ser Pro Ala Ala Ala Asn Asn Pro Leu Ala Tyr
            180                 185                 190

Lys Phe Ser Trp Asn Pro Ala Gly Ala Ile Arg Ala Gly Gln Asn Pro
        195                 200                 205

Ala Lys Tyr Lys Ser Asn Gly Asp Ile Ile His Val Asp Gly Lys Asn
    210                 215                 220

Leu Tyr Asp Ser Ala Ala Arg Phe Arg Val Pro Asn Leu Pro Ala Phe
225                 230                 235                 240
```

```
Ala Leu Glu Cys Phe Pro Asn Arg Asp Ser Leu Val Tyr Gly Glu His
                245                 250                 255

Tyr Gly Ile Glu Ser Glu Ala Thr Thr Ile Phe Arg Gly Thr Leu Arg
            260                 265                 270

Tyr Glu Gly Phe Ser Met Ile Met Ala Thr Leu Ser Lys Leu Gly Phe
        275                 280                 285

Phe Asp Ser Glu Ala Asn Gln Val Leu Ser Thr Gly Lys Arg Ile Thr
    290                 295                 300

Phe Gly Ala Leu Leu Ser Asn Ile Leu Asn Lys Asp Ala Asp Asn Glu
305                 310                 315                 320

Ser Glu Pro Leu Ala Gly Glu Glu Glu Ile Ser Lys Arg Ile Ile Lys
                325                 330                 335

Leu Gly His Ser Lys Glu Thr Ala Ala Lys Ala Ala Lys Thr Ile Val
            340                 345                 350

Phe Leu Gly Phe Asn Glu Glu Arg Glu Val Pro Ser Leu Cys Lys Ser
        355                 360                 365

Val Phe Asp Ala Thr Cys Tyr Leu Met Glu Glu Lys Leu Ala Tyr Ser
    370                 375                 380

Gly Asn Glu Gln Asp Met Val Leu Leu His His Glu Val Glu Val Glu
385                 390                 395                 400

Phe Leu Glu Ser Lys Arg Ile Glu Lys His Thr Ala Thr Leu Leu Glu
                405                 410                 415

Phe Gly Asp Ile Lys Asn Gly Gln Thr Thr Thr Ala Met Ala Lys Thr
            420                 425                 430

Val Gly Ile Pro Ala Ala Ile Gly Ala Leu Val Leu Ile Glu Asp Lys
        435                 440                 445

Ile Lys Thr Arg Gly Val Leu Arg Pro Leu Glu Ala Glu Val Tyr Leu
    450                 455                 460

Pro Ala Leu Asp Ile Leu Gln Ala Tyr Gly Ile Lys Leu Met Glu Lys
465                 470                 475                 480

Ala Glu
```